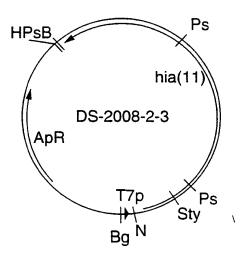
Restriction map of DS-2008-2-3, pT7 hia (11).



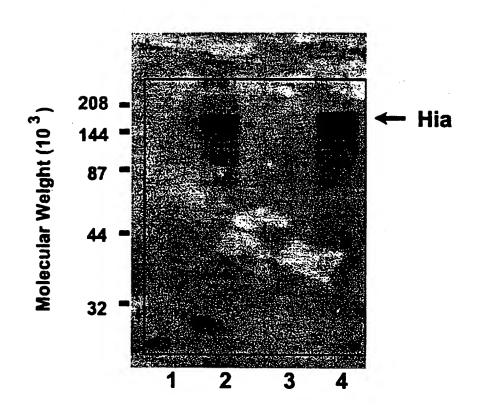
pT7 hia (11)

FIG.1A

Olig	Oligonucleotides used to PCR amplify the full-length strain 11 <i>hia</i> gene for expression studies.	ane for	expression	studies.
sense	Q)			
5,	Ecor I nde I		5038.SL	SEQ ID NO:2 SEQ ID NO:1
anti	antisense			
2,	K T G V A A G V G Y Q W * * AAAACAGGGGTTTGGTTTACCAGTGGTAATAG	3,		SEQ ID NO:5 SEQ ID NO:4
3,	TAA	2,	5039.SL	SEQ ID NO:3
	ECOR I BamH I			

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FIG.2



4/204
Construction of DS-2092-1 and DS-2092-40, plasmids containing tandem T7 hia (11) genes.

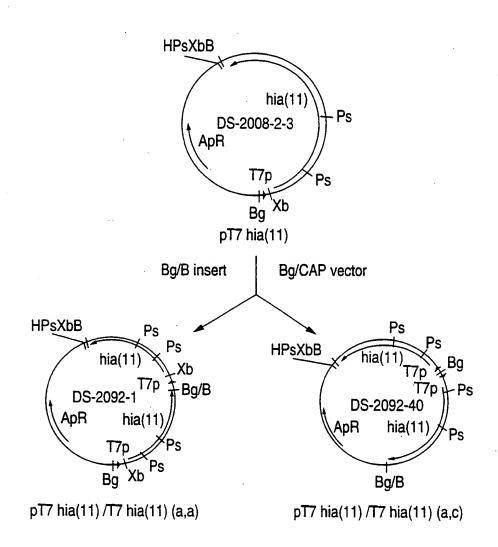


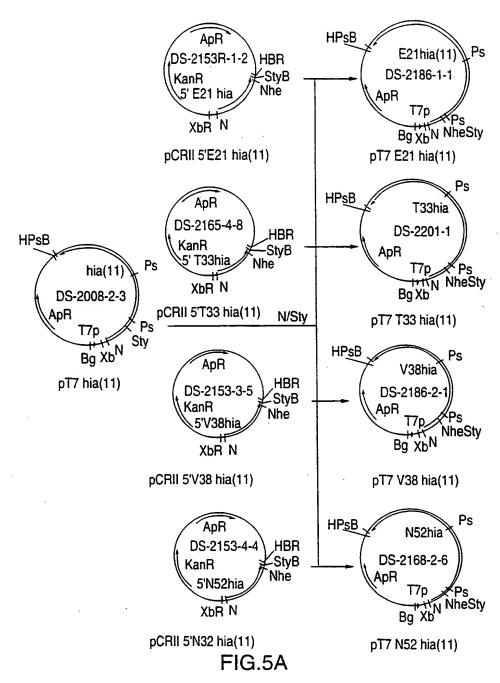
FIG.3

-1<u>G</u>.4

Sites for N-terminal truncations of rHia proteins.

ñ

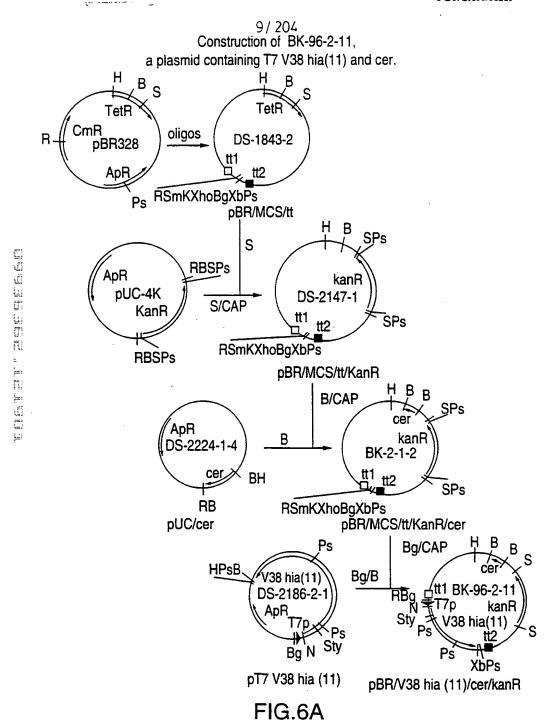
6/204
Construction of plasmids expressing truncated hia (11) genes.



	the state of the s	The complete force and the control of the standard of the stan	7	
FIG.5B	5B			
Oligon	Oligonucleotide primers to PCR amplify truncated strain $11\ hia$ genes.	11 hia ge	les.	
E21	Ecor I Nde I			
2,	M E L T R T H T K C A GOGAATTCATATGGAACTCACTCGCACCACCACAAATGGGCC	3,	5524.SL	SEQ ID NO: 8 SEQ ID NO: 7
T33			·	SEO ID NO:10
5,	OSCAATICATATGACCGIGGCGGTTGCCGTATTGGCAACCTG	3,	5525.SL	SEQ ID NO: 9
827				
5, 2	M V L A T L L S A T GGGAATTCATATGGTATTGGCAACG	3,	5526.SL	SEQ ID NO:12 SEQ ID NO:11

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o	1	Z	U	4

SEQ ID NO:14 L SEQ ID NO:13	SEQ ID NO:17 SEQ ID NO:16 L SEQ ID NO:15
5527.SL	5528.SL
M N T P V T N K L K A GGGAATTCATATGAATACTCTGTTACGAATAAGTTGAAGGCT 3'	isense H T I T F A L A K D L G CACACCATTACCTTTTGCGCAAAGACCTTGGTGG 3' GTGTGGTAATGGAAAACGCGATCGCTTTCTGGAACCACCCTAGGGG F A A A A A A A A A A A A A A A A A A



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PCT/CA00/00289

SEQ ID NO:50 SEQ ID NO:51

10/204

Oligonucleotides used to generate the multiple cloning site and transcription terminators for expression plasmids

T7 gene 10 terminator ATCTG.. OCTOGAGATICTICTIAGAC. COTCOGOCCEATTACTCOCCCCAAAAAACTTTAAGGGCCCATGCAGCTCTTACAG AATTIGCAGCCCCCTAATGAGCGGCCTTTTTTGAATTCCCGGGTA 😽 trpA terminator

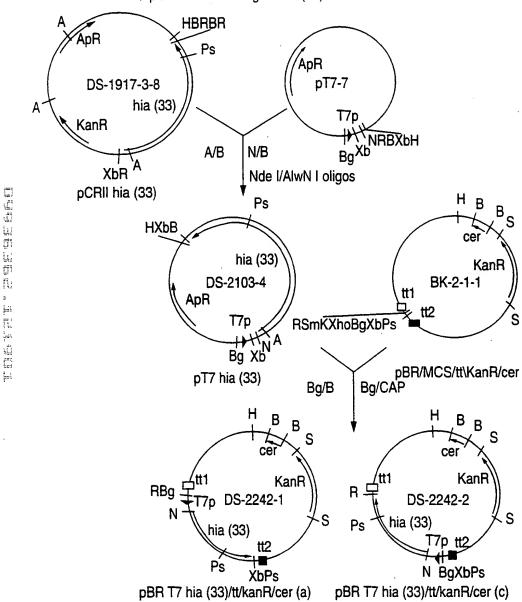
... ACCICIAIAICAACCACAAGICGITITITIGGGCAGITCIGGGCAAAIC

... TOCAGATATAGITICCTCCTTTCAGCAAAAAACCCCTCAA

GACCCGITTIAGAGGCCCCAAGGGGTITAIGCTAGTITATIGCTCAGCGGTGGCAGCAGCGTGCA TOCOGOGOTITOCOCCAATIACGATCAATIAACCAAGTCGCCACCGTCGTCGC

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11/204 Construction of DS-2242-1 and DS-242-2, plasmids containing T7 hia (33) and cer.



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FIG.7A

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TATICTGAACTCACTCGCGCCCACACCA...

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12/204

... AACGTGCCTCCGCAACCGTGGCAGCCG SEQ ID NO:52

SEQ ID 100:53

... TTGCACGGAGGCGTTGGCACCGTC

Ø A, ഗ Ø œ

SEQ ID NO:54 Ø

GAACCCGACAGCATAGACTTGAGTGAGCCCCCCCGTGTGCT

ACTIGITITIAAAAATIGCAATAAACCITIACAATACIGAGTTT

TATGAACAAAATTTTTTAACGTTATTTGGAATGTTATGACTCAAACTTG33CTGTCG

SUBSTITUTE SHEET (RULE 26)

Oligonucleotides used to generate the 5'-end of the strain 33 hia gene for expression studies.

13/2.04

Construction of DS-2340-2-3, a plasmid containing T7 V38 hia (33) and cer.

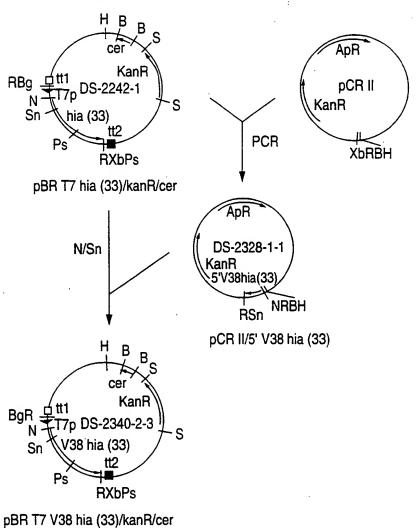


FIG.8A

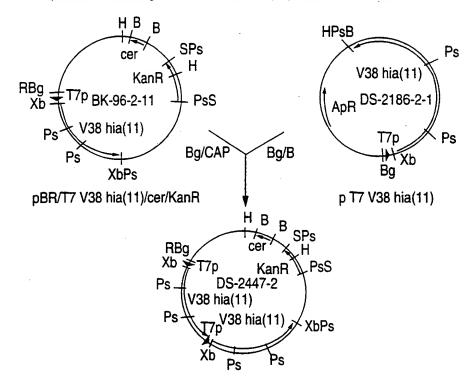
SnaB I site.

14/204

FIG.8B	FIG.8B	ene from the	V38 codon to	the SnaB I sit
sense				
٠	Nde I MVLATVLSAT			SEQ ID NO:61
5,	GGGAAITICAIAIIGGIAITIGGCGACCGIAITIGICIGCAACG	6286.SL		SEQ ID NO: 60
antisense	snse SnaB I			
ù	DETTATORY	3,		SEQ ID NO:20 SEQ ID NO:19
n m	CIGCITIOGICGGIIGGCAICCGIIAAAIGCAITITAACIICCAAGC	2,	6287.SL	SEQ ID NO:18

15/204

Construction of DS-2447-2, a plasmid containing tandem T7 V38 hia (11) cassettes and cer.



pBR T7 V38 hia(11)/T7 V38 hia(11)/cer/KanR

FIG.9A

16 / 204 Construction of DS-2448-17, a plasmid containing tandem T7 V38 hia(33) cassettes and cer.

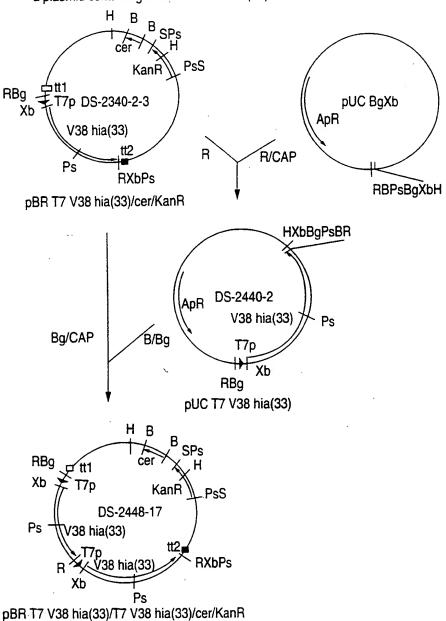
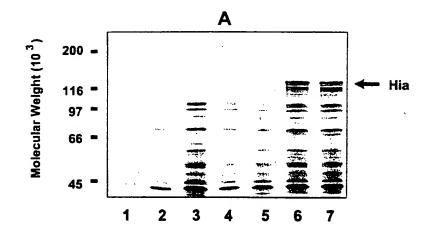
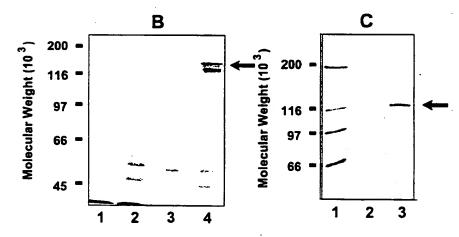


FIG.9B

17/204

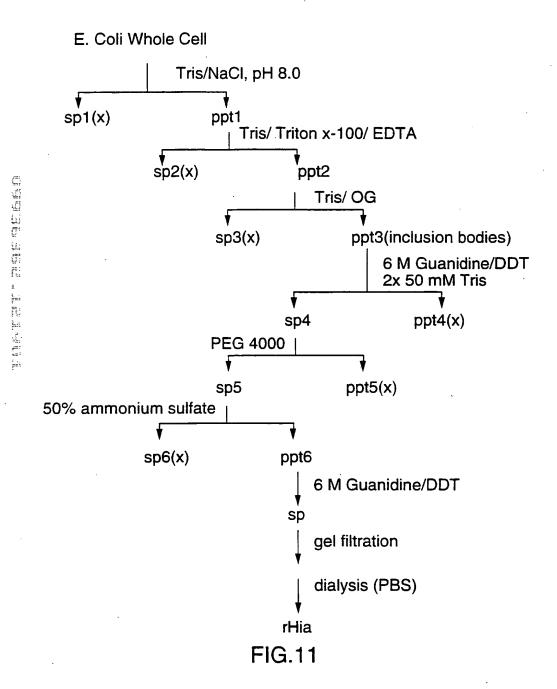
FIG.10



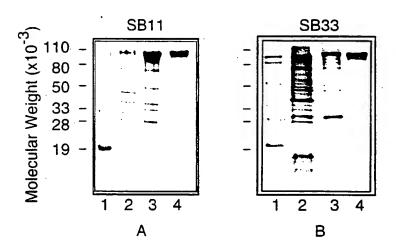


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18/204 Purification of rHia Proteins from E. coli



Purification of rHia (V38) from E. coli



- 1. Prestained molecular weight markers
- 2. E. coli whole cell lysate
- 3. Crude extract
- 4. Purified rHia protein

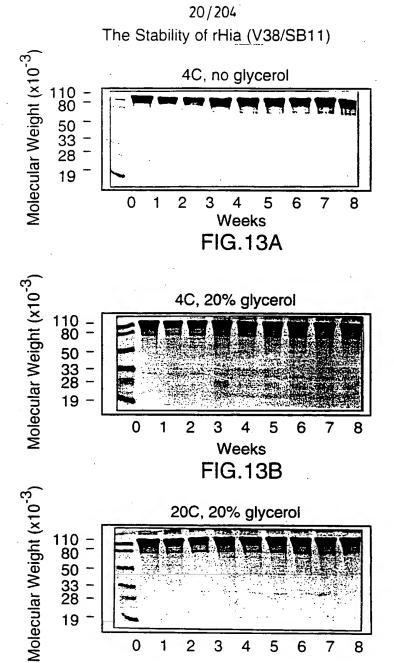
FIG.12

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Weeks FIG.13C

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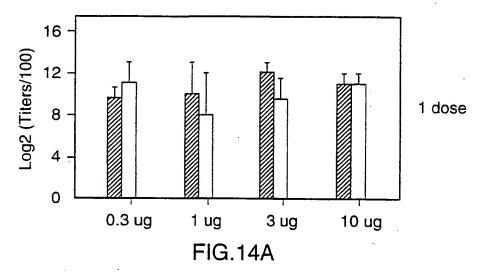
6

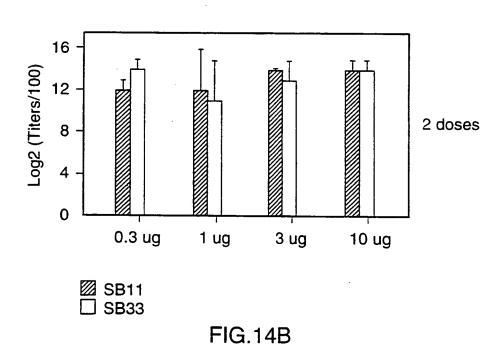
7

8

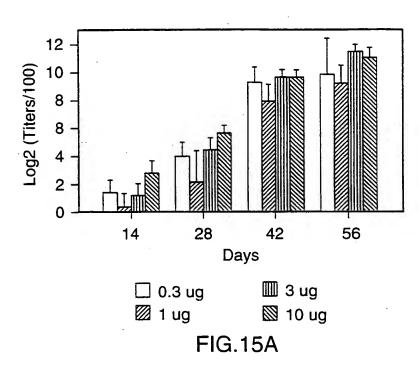
PCT/CA00/00289

Anti-rHia (V38) Antibody Titers in Mice

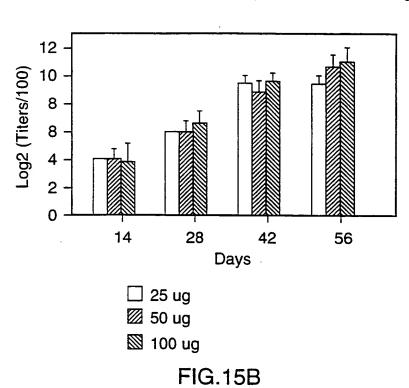




Anti-V38 rHia (SB11) Antibody Titers in BALB/c Mice

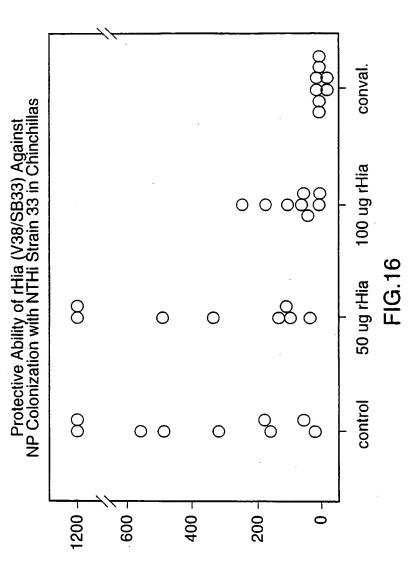


Anti-V38 rHia (SB11) Antibody Titers in Guinea Pigs



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cfu of Bacteria / 25 ul nasal wash

PCT/CA00/00289

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Oligonucleotides used to RCR amplify additional hia genes.

PCT/CA00/00289

GAATGTTTA 200

ACAAATAGTTT 190

GACAGGT

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NTHi strain 33 Hia

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E ME	A T G		ALA	GCA			GLY	0 g c	
167	G T T		SER	T C C			ALA	GCA	0
180	AAT		ALA	G C C T 110			SER	A G T	170
ą	T G G		ARG	C G T			ALA	9 0 0	•
. [2 1	ATT		LYS	AAA	•		GLN	CAG	
167	G T T		開	A C C 100			VAL	GTT	160
IGAACAA Dur acan var tie mee acan var meen mee can	AAC	E :: :	ARG ALA HIS THR LYS ARG ALA SER ALA THR VAL	CAC	 [EQ. : . :	: :	SER ALA THR VAL GIN ALA SER ALA GLY SER THR	ACG	
A C A	TTT	LEU,	ALA	ນ ນ ນ <u>ຍ</u>	VAL	TAT	ALA	GCA	
	AATTTTAACGTTATTTGGAATGTTATGACTCA 30 40 60	ALA VAL VAL SER GLU LEU THR GCTGTCGTATCTGAACTCAC 70 80	ARG	TCGCGCCCACAAACGTGCCTCCGCAACCGT	ALA VAL LEU ALA THR VAL LEU	GCTGTATTGGCGACCGTATT 130 140	SER	GTCTGCAACGGTTCAGGCGAGTGCAGGCAGTAC	150
A A A A 20	A	SER CTG	:	. :	ALA	C G A 140	:		:
TAA		VAL TAT			DET!	T G G			
AAA		VAL 1 T C G			VAL	TAT			
10 10		ALA CTG 70			ALA	C T G			
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GAATTCG		THR TRP AACTTGG			ALA ALA	GGCAGCC			
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	GLY	GGT	47				ASIN	AAT	530				LYS	AAG	23
	ASP	GAC					ALA	909					GLY	C C C	
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**	CLY	ပြင	460				ALA	0 C C	520				ALA	GCA	280
:	PHE GLU GLY LYS ASP GLY VAL THR VAL	GTTGTTTGAAGGCAAAGACGGTGTAACGGTTAC		IHR	: C	:	VAL THR PHE ALA LEU ALA ASN ASP LEU ASN VAL	CGTTACTTTGCCCTTGCGAATGACCTTAATGT		 EQ.	Ξ.	:	SER LEU GLY ALA ASN GLY LYS LYS VAL ASP	ATCGCTTGGTGCAAACGGCAAGAAGTCGATAT	
	铝	ТТТ		HIS	ACA		出	ACT		LYS 1	AAT		Per	C T T	
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ACACCTTACAAAAGAAATCAGCGATAC... H OFF OFF LYS

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...AGAACGTAACCGTGCGAGCGTGGGCGATGT ... 750

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ATTGAATGCGGGTTGGAATATTCGTGG...

...CGCAAAACGATTGGCGGTACAGTGGATAATGT ... 810 820 830 840 GLY THR LYS ALA 810

GAAAGTGGGCAATGAGTATTACGAAGC

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CAATATGTTACGGAAGACAGCAAAAC...

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	GLU PHE ALA SER GLY ALA ASN ALA ASN VAL SER TGAATTTGCCAGCGCCAAACGCAAATGTGAG					THR VAL ARG VAL ASP VAL THR GLY LEU PRO VAL	A A C C G T C C G T G T G T G T A C A G G C T T G C C G G T	
	GLY 3 G C (٠	ASP	3 A T (
	SER AGC(880				VAL	3 T G (940
: :	ALA 3 C C 7		完	:	:	ARG	GTC	
GTTTCAACTTATGACACTGT 850 860	PHE FT(THR ASP ASP ASN LYS LYS THR	ACTGATGATAACAAAAAAC		VAL	TC	
A C A	GLU 3 A A 3	370	YS L	AAA		THR	CCC	30
A T G 8	T	870	Na Na	CA	920	:	A A	930
T T A			Æ	TAA				
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ТGАТТТТ			VAL THR	GTT,				
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CAAGCAAGACGGTTCGGCGGATATGGA... ...CGTTGTC ASP GLY GIN

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LYS LYS VAL GLU ASN GLY LYS LEU ALA LYS THRTAAAAAAGTCGAAATGGCAAGCTGGCGAAAAC1050 1060 1060 1070 1080	LYS VAL LYS LEU VAL SER ALA ASN GLY TAAAGTGAAATTGGTATCGGCAAACGG 1100 TAAAGTGAAATTGGTATCGCAAACGG 1100 THR ASN PRO VAL LYS ILE SER ASN VAL ALA ASPTACAAATCCGGTGAAAATCAGCAATGTTGCGGATACAAATCCGGTGAAAATCAGCAATGTTGCGGA1110	GLY THR GLU ASP THR ASP ALA VAL SER CGGCACGGAAGATGCGGTCAG 1150 PHE LYS GIN LEU LYS ALA LEU GIN ASP LYS GIN PHE LYS GIN LEU LYS ALA LEU GIN ASP LYS GIN TTTAAGCAGTTGAAAGCAGAAGATAAACA 11200 1170 1170	VAL THR LEU SER ALA SER ASN ALA TYR GGTTACGTTAAGCTTA 1210 ALA ASN GLY GLY SER ASP ALA ASP GLY GLY LYSTGCCAATGCGAGGGGGGCAA 1260

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E	.: T	:	LYS	AAA		
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THR LEU GLY ASN ASP	3 G C 7	1280	:	9	:	
邑	TTA					
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ALA	GGCAACTCAAACTTTAGGCAATGATTT					

GTTGAACATCAAAGCAGCAGGTGACAC ...

ASP

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開	A C C			THR 1	C G A		ASP
VAL	GTT	1350			C T A		GIN
:	 G	:		LYS ALA	AGG	1400	:
				GLY 1	GTA		
				ASP (T G		
				AS	GA		
				GLY ASP	GAT	1390	•
					3 g g		
				VAL	GGTTGGCGATGATGGTAAGGCTACGA		
					ß		

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GLU ALA SER GLU LEU VAL ASP SER LEU... TGAGGCTTCTGAATTGGTTGACAGCCT...

GLY

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...AAAGAGCGTGGAGTTTAAAGACACGGAGAATGG

33/204

	55	7 204	
ASN LYS LEU GLY TRP LYS VAL GLY VAL GLY LYSGAACAAATTGGGCTGGAAAGTGGGCGTTGGTAA1470 1480 1490 1500	ASP GLY THR GLY ALA THR ASP GLY THR AGACGGCACAGGACGATGGCAC 1510 HIS THR ASP THR LEU VAL LYS SER GLY ASP LYSGCATACGACACTTTAGTGAAGTCGGCGATAAGCATACCGACACTTTAGTGAAGTCGGCGATAA1530	VAL THR LEU LYS ALA GLY ASP ASN LEU A G T A A C T T T G A A G C C G G C G A T A A T C T 1570 1570 LYS VAL LYS GIN GLU GLY THR ASN PHE THR TYR G A A G T C A A A C A A G A G G T A C A A A C T T C A C T T A 1620 1620	VAL LEU ARG ASP GLU LEU THR GLY VAL CGTGCTCAGAGATGAATTGACGGGCGT
	A G	A G	၁ ဗ

FIG. 18H

LEU LYS LIS FILL CL. CTGAAGAAATTTGGTGATGCGAA

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CGGGTAATAAGCAGTTAAAAACGT ...

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		PRO	$C \subset G$	00				ASP .	GAC	0
		TH	ACG	1730				SER	TCA	179
		LYS ASP GLY LEU THR ILE THR PRO ALA ASN ASP	CAAAGACGGCTTGACCATTACGCCGGCAAACGA					ALA	GCT	1770 1780 1790 1800
		THR	ACC					VAL	GTG	
		TEG	T T G	1720				LYS	AAA	1780
: :	:	GLY	0 G C		ALA	: c	:	ILE	ATT	
ТТА		ASP	GAC		ASP	A T G		LYS	AAG	
AGA		LYS	AAA	1710	THE	CTG		ASP	GAC	1770
GTGCAAGCACGAAGATTAC	1700	:	 	1710	ALA ASN GLY ALA ALA ALA THR ASP ALA	STGCGGCGGCGACTGATGC	1760	:	$T \cdots T$:
GCA					ALA	555				
CAA					ALA.	990				
GTG	1690				I.Y		.750			
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A A					ASA	A A				
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LYS ' A A 1920	ASN 2 A A 1980	THR , A C 2040	LYS : A A 2100
ALA TYR LYS ; C C T A T A A 1920	ASP GAC	ASP LYS 3 A C A A A 2	PHETTC
ALA G C C	ALA G C T (ASP G A C	LYS A A A
ASN A A T (VAL	ALA S C A (VAL 3 T G
ASP AS ACA 1910	THR VAL 1 C C G T T 1970	SER ALA CTGCAC 2030	GLU V 2090
IYR A T G	PRO	ILE \TTT	ASN A T G
JIN , A A T	THR	VAL 3 T C A	ALA ASN GLU VAL LYS PHE LYS CCAATGAAGTGAAATTCAA 2090 2100
LYS (A A A A A A A A A A A A A A A A A A A	GLN ' CAAA 1960	TRP 15 G G G 2020	ASN 7
ASN LEU THR LYS GIN TYR ASP ASN ALA TYR LYSCAACTTAACGAAACAATATGACAATGCCTATAA 1920 1920	ASN LEU ASP GLU LYS SER A A T C T G G A T G A A A A A G 1940 LYS GLY LYS GLN THR PRO THR VAL ALA ASP ASI T A A A G G C A A G C A A C T C C G A C C G T T G C T G A C A A C T C C G A C C G T T G C T G A C A A C T C C G A C C G T T G C T G A C A A G G C A A G C A A A C T C C G A C C G T T G C T G A C A A G G C A A G C A A A C T C C G A C C G T T G C T G A C A A G G C A A G C A A A C T C C G A C C G T T G C T G A C A A G G C A A G C A A A C T C C G A C C G T T G C T G A C A A G G C A A G C A A A C T C C G A C C G T T G C T G A C A A G C C A A G C A A A C T C C G A C C G T T G C T G A C A A G C A A G C A A A C T C C G A C C G T T G C T G A C A A G C C A A G C A A A C T C C G A C C G T T G C T G A C A A G C C A A G C A A G C A A A C T C C G A C C G T T G C T G A C A A G C C A	THR ALA ALA THR VAL GLY ASP LEU ARG ACCGCTGCAACCGTGGGCGATTTGCG 1990 GLY LEU GLY TRP VAL ILE SER ALA ASP LYS THF CGGTTTGGGCTGGGTCATTTCTGCAGACAAAC CGGTTTGGGCTGGGTCATTTCTGCAGACAAAAC	THR GLY GLU SER LYS GLU TYR SER ALA A C A G G C G A G T A T A T A G C G C 2050 GIN VAL ARG ASN ALA ASN GLU VAL LYS PHE LYS G C A A G T G C G T A A C G C C A A T G A A A T T C A A 2050 2100
	THR A C C A 1930	ALA 3 C A A 1990	GLU 3 A G T 2050
	LEU THR LTGAC 193	ALA ALA SCTGC 2	THR GLY GLU CAGGCGA 205
	GLY LEU THR GGCTTGACC 1930	THR A C C G	THR ACAC

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SER GLY	LYS THR LEU ASP ASN GLY THR ARG GLU ILE THRTAAAACATTGGATAACGGTACGCGAAATTAC 2130 2140 2140 2150	SP GLU ASN ALA 1 CGAAAATGC 2180 ILE ALA PHE GLY SER GLY SER LYS ALA LEU ARGCATTGCTTTCGGTTCTGGCTCAAAGCCTTGCG2190 2220	E GLY THR GLY TGTACGG
SER GLY ASN GLY ILE ASN VAL SER GLY GAGCGCAACGTATCAATGTTCCGG 2110 2120	LYS T A A A 2130	THE GLU LEU ALA LYS ASP GLU ASN ALA LITTTGAATTGCTAAAGACGAAAATGC 2170 2180 ILE ALA PHE CATTGCTTTC 2190	ASP ASN THR VAL ALA ILLI CGATAACACGGTGGCGAT 2230

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ASN ' A A 2340	LYS ALA A A G C 2400	~	LYS . A A 2520
ASP GATA 23	LYS A A A	THRACT	ASN LYS AATAA 2520
ALA PHE GLY ASN CTTTCGGTAACO 2330	TYR T A T	GLU 3 A G V	GLY 3 G T 1
GLY 3 G T	LYS A A A A	LYS A A A A (LEU T T G (
PHE GI LTCG(2330	ALA L3 3 C G A 7 2390	GLY E GGTA.	TYR LEU GLY TATTTGGGT 2
ALA 3 C T 1	GLY VAL ASN ALA LYS TYR 3 G A G T T A A T G C G A A A T A T 5 2380 2380	ASP 3 A C (VAL 3 T T T
SER TYR IGCTACO 2320	VAL 3 T T ?	LYS A A A C	SER 「CCC
SER A G C 7 2320	GLY G G A (2 G A (ASP 3 A C <i>1</i> 2440	ASN A C 7
ALA GLY GLY SER TYR ALA PHE GLY ASN ASP ASI AGCCGGTGGCAGCTACGCTTTCGGTAACGATAA 2310 2320 2340	N THR PHE VAL A C A C T T T G T 2360 LEU GLY ASN GLY VAL ASN ALA LYS TYR LYS ALAG T T G G G T A A T G G A G T T A A T G C G A A T A T A A A G C 2370 2400	R GLU THR VAL 2GGAAACCGT 2420 THR VAL LYS ASP GLY LYS GLU THR THEAACTGTTAAGGACAAAGACGGTAAAGAGACTACAACTGTTAAGGACAAAGACGGTAAAGAGACTACAACTGTTAAGGACAAAGACGGTAAAGAGACTAC	A LEU GLY ALA CGTTAGGGGC 2480 THR VAL GLU ASN SER VAL TYR LEU GLY ASN LYS TACGGTTGAAAACTCCGTTTATTTGGGTAATAA TACGGTTGAAAACTCCGTTTATTTGGGTAATAA
GLY GGT	PHE TTGGIN	THR VACG	JLY PGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
ALA G C C 310	THR BACTTO DO LEU LEU 2370	GLU 1 G A A A 0 THR A A C T 2430	ALA LEU GLY CGTTAGGGC 2480 THR VALTACGGTT
ALA A G C 2310	ASN 7 2360 2360G	THR (C G G 2420 A A 2	LEU CGTTA 2480 THE
	LYS A	ASP 1 3 A T A 5	LYS P
	SER I	VAL A	PRO LCTA
	SI T T (V7 0	
	THR A C ' 235	ASP G A '	VAL G T ' 247
	ILE A T T	GLY G G A (THR VAL ACTGT' 247
	ARG ILE THR SER LYS ASN THR PHE VAL CCGTATTACTTCTAAAACACTTTTGT 2350 2360 LEU GLY ASNCTTGGGTAAT	ASN GLY ASP VAL ASP THR GLU THR VAL CAATGGAGATGTTGATACGGAAACCGT 2410 2420 THR VAL LYSAACTGTTAAG	VAL THR VAL PRO LYS ALA LEU GLY ALA CGTTACTGTTCCTAAAGCGTTAGGGGC 2470 THR VAL GLUTACGGTTGAA
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FIG. 18M

TCGACTGCGACAAAAGATAAGGTAA ... GLY

...AAATCTGAAGTGGTACGGCGGGTAACAC LYS ASN LEU ... 2550

ASN

GLY

THR ALA

GLY

TACAACTGCTGGTACAACGGGTACGGT... GLY 2600 GLY ALA

...AAACGGCTTTGCCGGTGCAACGCCACGGTGC

38/204 ALA

> GTTTCTGTCGGCGCAAGCGGCGAAGA... GEO.: GE GLY ALA GLY Ŕ

... ARG

...AAGACGTATCCAAAACGTTGCGGCAGGCGAAAT ... 2670

GEU

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ILE

THR ASP ALA ILE ASN... TCCGCTACTTCCACCGATGCGATTAA.... SES

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G C G	ALA G C A	SER	SER
LYS A A A	THR ACAC	VAL G T T	ILE A T T
ALA G C A 0	ALA GLY CAGGT 7	MET ATG	SER ARG
TYR ALA VAL ALA LYS LATGCCGTGGCAAAA 2750	ALA GGCAG	SER MET TCAATG 2870	SER T C A
ALA G C C	ALA ASP 3 C A G A T	LYS A A A	VAL 3 T A
TYR T A T	ALA G C A	SER GLY LYS CCAGGTAAA 2860	GLY G G G G
LEU T T G 1 2740	ARG C G T G 2800	SER T C A 2	ILE A T C
SER GIN AGCCAGT	LYS A A LYS . A A A	JAN A MET A.T.G.'	EX GIN SER G T C A A A G GLY LEU ALA ILE GLY VAL
SER AGC	ASN IN A TA A GLY GGC	PRO GIN CACA SER MET TCTATG	SIN SAAAAAAATTA
GLY SER GIN LEU TYR ALA VAL ALA LYS GLYCGCCAGCTGTATGCCGTGCCAAAGGG 2730 2740	N VAL ASN LYS A G T G A A T A A 2780 VAL GLY LYS ARG ALA ASP ALA GLY THR ALA A G T G G C A A A C G T G C A G A T G C A G G T A C A G C A 2790 2790		GIN GLY GIN SER 2 A A G G T C A A A G 2900 GLY LEU ALA ILE GLY VAL SER ARG ILE SER T G G T T T A G C T A T C G G G T A T C C C
GL) C G G 2730	GIN VAL 2 A A G T G <i>P</i> 2780 VAL G T G	SER GIN LEU C A C A G T T A C 2840 AİAA G C CA G C C	GLN (2900 2900T
	GLY 3 G A C	SER CCAC	TYR [ATC
	ALA 3 C T (ALA 3 C T 3	SER AGT7
	LEU CTT (2770	ALA 3 C G (2830	SER A G T 7 2890
	THR ASN LEU ALA GLY GIN VAL ASN LYS A C A A G T G A A T A A 2770 2780 VAL GLY LYS VAL GLY LYSA G T G G C A A A	ALA LEU ALA ALA GCATTAGCGGCT 2830	ALA GLY SER SER TYR GIN GLY GIN SER GCGGAAGTAGTTATCAAGGTCAAAG 2890 2890 GLY LEU ALA
	THR ACAA	ALA G C A	ALA G C G ·

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	LY LYS VAL ILE ILE ARG LEU SER 3 C A A A G T G A T T A T T C G C T T G T C 2950 GLY THR THR ASN SER GLN GLY LYS THR GLY VAL A G G C A C A A T A G C C A A G G T A A A A C A G G C G T 2970 2980 2990	LA GLY VAL GLY TYR GLN TRP *** C A G G T G T T A C C A G T G G T A 3010 3020
٠	S VA G T S O S O S O S O S O S O S O S O S O S	$egin{array}{ccc} Y & V_F \ T & G & T \end{array}$
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20 MET ASN LYS ILE PHE ASN VAL ILE TRP ASN A A T G A A C A A A T T T T T A A C G T T A T T G G A A	THE VAL VAL SER SGGTTGTCGTATC 80	: : \$100
3(SYS AAA	40 L SH A T (90 IFFR C T C	n ALA GGC
N I	CGTCGT	, LE A T T
GAZ	VAL GT GT ACT	VAL G T
20 MET	VAL 3GTT 80 . GLU	ALA G C C
: 2	TRP TGG 8	VAL A GTTG
	THRACT	ALA G C A
	GLN C A A	VAL G T G
10	AL VAL THR GIN THR TRP VAL VAL VAL SER TIGIGACICAAACTIGGGTIGICGTATC 80 90 GLU LEU THR ARGTGAACTCGC 100	THR A C C
	VAL 3 T G	ALA 3 C C
	VAL VA TGTTGT	SER ALA THR VAL ALA VAL ALA VAL LEU ALA

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TTGTCCGCAACGGTTCAGGCGAA 160 170 180 150 ... SE GLU GLU... LEU E ...AACCCT ASP THR ASP 140 GEU ASN GLU 130 ASP 混

TGCTACCGATGAAAACGAAGATGATGAAGA... 210 ...

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LEU T T 240	VAL			LYS A A 360		LYS
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ARG CGC1	THR	A 0		ILE A T C		SER
GLN P	CILY	3 G A A 290		THR 3		TYR
GLU LEU GLU PRO VAL GIN ARG SER AGAGTTAGAACCCGTACAACGCTCT 230	CLU	A C T G G A G A A C A A G A G G G A A C A A C A G G G T 280 280 300		ALA VAL GLY SER SER THR ILE THR GCAGTAGGAAGCAGCACAATCACC 340		THR
PRO	GLY G G 270 GLN	AAG	ASN A A 330	SER AGC?	SER A G	PHE
GLU 3 A A C 220	LYS SER ALA LYS GLU GLY A A A T C C G C T A A G G A A G G 260 270 THR GLY GLU GIN	280 280	GLY A	VAL GLY FTAGGAP 340	GLN S	ASP
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GLU GAG	ALA I CTA THR	A C T	SER CAT	ALA G C A (ILE TCA	GLY
. 4 : : :	SER A 1 C C G 260		T T 320		3 A A A 380	3 :
	SE T C T .	• •	ASP G A T		LYS A A A	•
	LYS A A A		THR A C A		LEU CTG	
	PHE I T C		ASN A A C		ASN A A C	
	SER A G C 1 250		LEU LTG 7 310		ASP 3 A C 7))
	TRP GG 2		ASN A A T 1		GLY 3 G C (
	ARG TRP SER PHE A G G T G G A G C T T C 250		TILE ASN LEU ASN THR ASP SER GEN ASN ATAAATTTGAACACAGATTCATCAGGAAA 310 320		ALA GLY ASP ASN LEU LYS ILE LYS GIN SER GCCGGCGACAACTGAAATCAAACAAG	

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			GLY.) D 5 :	470				黑	CAC	530				開
			PE	TTC					LYS	AAA					
展	:	450	GLU LYS LEU SER PHE GLY ALA ASN GLY ASN	TGAAAATTATCGTTTGGCGCAAACGGCAA		LY	 G	510	LEU LYS LEU ALA LYS THR GLY ASN GLY ASN	CTTGAAATTGGCGAAAACAGGTAACGGAAA		LY	.: G	570	ILE ALA SER THR LEU
GLU LEU LYS ASN LEU THR SER VAL GLU THR	AAA	45	E	TTA	460	LYS VAL ASP ILE THR SER ASP ALA ASN GLY	TTGATATTACCAGTGATGCAAATGG	51	LEU	TTG(520	ASIN G	ACG	57	SER
WAL (T T G		LYS	AAA		ALA 1	CAA		LYS	AAA		LEU A	TAA		ALA
SER.	G T G		GLU	GAA		4SP	ATG		LEU	T T G		IIS 1	ACT		ILE
THE	CCA	440	:		:	SES.	GTG	200	:	.: :	:	WAL	TTC	260	:
rear Rear	T G A					景	CCA					ASIN	ATG		
ASIN	ACC					· · 田田	TTA					SER	GTA		
LYS	AAA	430				ASP	ATA	490				ASN	ACA	550	
LEU LEU	T G A					VAL.	TTG					SIN	AAA		
CIN	AGAGCTGAAAACCTGACCAGTGTTGAAAC			•		LYS	TAAAG1					GLY GIN ASN SER ASN VAL HIS LEU ASN GLY	TGGTCAAAACAGTAATGTTCACTTAAACGG		
													-		

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FIG. 19D

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...TGTCCGTGTGGATGTAACAGGCTTGCCGGT

VAL

GLY LEU

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...CATTGATGCGGTTAATTATCATCGCGCTGC 099 ...GAATATCCAAGGCAATGGAAACAATGTCGA ALA ARG HIS TYR GLY ASN VAL AAGCGTACAAGATGTGTTAAACAGCGGTTG... GLY GIN ASP ILE ... ASN ASIN E

GIN

TACGGCTGATACGGCTCACAAAAAGACAA ... HIS LYS LYS ALA

...TGTCAATGGCGCGAATGCCAATGTGAGCGT

WAL

ASIN

ASIN ALA

ALA

VAL ASIN GLY

ASP THR VAL ASP PHE...

TTTTGTCCGTACTTACGACACCGTGGACTT...

TYR

ARG THR

ASP VAL ARG VAL

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ASP

ALA

VAL

SER ASIN

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SER PHE...

THR ASP ALA VAL

ASP

GEU

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GLY

CGGCACGGAAGACACGGATGCGGTCAGCTT ... 1030 1030 1040

...AAATCCGGTGAAAATTAGCAATGTTGCAGA

FIG. 19E

GIN TYR VAL THR GLU ASP GLY LYS THR VAL	860 870 VAL LYS VAL GLY ASN GLU TYR LYS ALA	TGTGAAAGTGGCCAATGAGTATTACAAAGC 880	LYS ASP ASP GLY SER ALA ASP MET ASN GLN CAAAGATGACGGTTCGGCGGATATGAATCA 910 920 930 LYS VAL GLU ASN GLY GLU LEU ALA LYS THRESAAAAGTCGAAAACGGCGAAAAC
TR GLU ASP GLY LYS THE	Secretary Secretary William Wi	T G T G A A A G 1	JY SER ALA ASP MET ASN STTCGGCGGATATGAA 920 LYS VAL GIAAAAGTCG
GIN TYR VAL TH	850		LYS ASP ASP GL CAAAGATGACGG 910

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GLN C A 1080	r0	$\overline{}$	GLN C A 1260				
LYS A A A (GLY GGC 1	GLU G A G	VAL G T A				
ASP 3 A C I	GLY G G C	GLY G G C (SER T C G				
GLN C A A (ASP 5 A C	ASP 3 A T (GLY 3 G T				
LEU G F T G C 1070	ASN PASN A A C G	SER 1 1190	LYS (A A A G 1250				
LYS GIN LEU LYS ALA LEU GIN ASP LYS GIN TAAGCAATTAAAAGCCTTGCAAGACAACA 1060 1070 1080	R ASN ALA TYR ALA CAATGCTTATGC 1110 ASN GLY THR ASP ASN ASP GLY GLY LY CAATGCGGTACAGATAACGACGGCGCAA 1120	R ASN GLY LEU ASN C A A T G G T T T G A A 1160 PHE LYS PHE LYS SER SER ASP GLY GLU LE T T T T A A A T T T A A A T C T A G C G A T G G C G A G T T T A A A T C T A G C G A T G G C G A G T T T A A A T C T A G C G A T G G C G A G T T T A A A T C T A G C G A T G G C G A G T T T A A A T C T A G C G A T G C G A G T T T T A A A T C T A G C G A T G C G A G T T T T A A A T C T A G C G A T G C G A G T T T T A A A T C T A G C G A T G C G A G T T T T A A A T C T A G C G A T G C G A G T T T T A A A T C T A G C G A T G C G A G T T T T A A A T C T A G C G A T G C G A G T T T T A A A T C T A G C G A T G C G A G T T T T A A A T C T A G C G A T G C G A G T T T T A A A T C T A G C G A T G C G A G T T T T A A A T C T A G C G A T G C G A G T T T T A A A T C T A G C G A T G C G A G T T T T A A A T C T A G C G A T G C G A G T T T T T A A A T C T A G C G A T G	R GLY ASP THR VAL CGGCGATACGGT 1220 1230 THR PHE THR PRO LYS LYS GLY SER VAL GLATACTTTACGCCGAAAAAGGTTCGGTACA 1240 1250				
LYS A A A G	LA C O THR A C A G	IN	AL T J PRO				
LEU FTAA 1060	TYR ALA A T G C 1110 GLY THR G G T A C A 1120	ASN GLY LEU ASN A A T G G T T T G A A 1170 PHE LYS PHE LYS T T T A A A T T T A A A T	THR VAL 1 C G G T 1230 THR PRO A C G C C G 1240				
I A T	TY TY A T A C G	LE TT TT S 1	THAC				
LYS GIN A G C A A T	SN ALA A T G C T ASN GLY A A T G G C	SN GLY ATGGT: PHE LYS	ASP G A T PHE				
LYS	ASN A A T G ASN ASN ASN ASN	ASN A A T D PHE	THR GLY ASP 1 C C G G C G A T I 1 L 2 O THR PHE TA C T T T T				
	LEU SER THR SER ASN ALA TYR ALA T T G A G C A C G A G C A A T G C T T A T G C 1090 1100 ASN GLY GLY THR C A A T G G C G G T A C A 1120	GIN THR LEU SER ASN GLY LEU ASN C A A A C T T T A A G C A A T G G T T T G A A 1150 1160 1170 PHE LYS PHE LYS T T T T A A A T T T A A A T T T A A A	ILE SER ALA THR GLY ASP THR VAL A T T A G C G C G A C C G C G A T A C G G T 1210 1210 THR PHE THR PRO TA C T T T A C G C C G 1240				
	THR ACGA	LEU LTA?	ALA 3 C G 7				
	SER A G C A	THR A C T T	SER G C G				
	LEU 'TGA 1090	GLN : A A A A A 1150	ILE 1 T T A 1210				
•	T A T	A A	T & D				
	VAL THR GGTTACG	ALA THR GGCAACT	LEU LYS G T T G A A A				
•	O	O	Ö				

FIG. 19G

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AGTAACTTTGAAAGCCGGCGACAAT 1450 1460

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VAL GLY ASP ASP GLY LYS ALA SEK ILE SEK GGTTGGCGATGATGCTTCAATTTC 1270 1280LYS GLY ALA ASN THR THR GLU GLY LEU VALAAAAGGTGCAAATACAACTGAAGGTTTGGT 1320	GLU ALA SER GLU LEU VAL GLU SER LEU ASN TGAGGCTTCTGAATTGGTTGAAAGCCTGAA 1330 1340 1350 LYS LEU GLY TRP LYS VAL GLY VAL GLU LYSCAAACTGGGTTGGAAAGTAGGGGTTGAGAA 1380	VAL GLY SER GLY GLU LEU ASP GLY THR SER AGTCGGCAGCGAGCTTGATGGTACATC 1390 1400 1400 1410 LYS GLU THR LEU VAL LYS SER GLY ASP LYSCAÄGGAAACTTTAGTGAAGTCGGGCGATAA

GLY

THR ASP ALA ASP...

TGCGAATGGTGCGACGGTGACTGATGCCGA ... THR

ALA

...CAAGATTAAAGTTGCTTCGGACGGCATTAG

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VAL LYS GIN GLU GLY THR ASN PHE THR TYR GGTCAAACAGGGCACAAACTTCACTTA 1480 1490 1500	AIA LEU LYS ASP GLU LEU THR GLY VAL LYS CGCGCTCAAAGATGAATTGACGGGCGTGAA 1510 1510 SER VAL GLU PHE LYS ASP THR ALA ASN GLYGAGCGTGGAGTTTAAAGACACGGCGAATGG	ALA ASN GLY ALA SER THR LYS ILE THR LYS TGCAAACGTGCAAGCACGAAGATTACCAA 1570 1580 1590 ASP GLY LEU THR LEU ALA ASN GLYAGACGGCTTGACCATTACGCTGGCAAACGG
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SIN VAL LYS GIN AIA ASP GIU VAL LEU PHE A A G T A A A A A G C T G A T G A G T T C T C T T T 430 440 450	THR GLY SER GLY ALA ALA THR VAL SER SER A C T G G A T C T G G T G C T G G T T A G T T C C 470 480	CTAAAGACGGTAAACATTACC CTAAAGACGGTAAACATTACC 490 IIE SER VAL THR LYS GLY SER PHE ALA GLU SER PHE PHE ALA GLU SER P	A A A C T G A A C T A C T G G A G G T C A A A A A C T G A A C T G G A G G T C A A 550 VAL ASN ALA ASP ARG GLY LYS VAL LYS ALA G T A A A C G C C G A C C G T G G T A A A G C C T 580 500
GIN VAL LYS CAAGTAAA		SER SER LYS AGCTCTAA	VAL LYS THR GTAAAAAC

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LYS A A G 660	ASN A A T	54/204 P C C A C C	PHE
ALA G C T	GLU GAA	LEU TTA	雅
VAL GTT	ILE ATT	THR	VAL
ASP G A T 650	ASP G A C	ASP G A C 770	SER
LYS A A A	ASP G A T	GECC	ГУS
VAL G T A	ASP G A T	ALA G C A (GLY
THR ACT 0	LYS A A A 690 THR	ASP 3 A C 750 1 LYS C A A A (760)	LYS 4 A G 810
LYS VAL ALA THR VAL LYS ASP VAL ALA LYS A A A G T T G C A A C T G T A A A A G A T G T T G C T A A G 640 650 650	L G 7 SER	GET GCT GCAGGCAAAATGAAACTACAGAC GGTGCTGCAGGCAAAATGAAACTACAGAC 730 740 750 GIN ALA LEU LYS ALA GLY ASP THR LEU THR CAAGCTCTCAAAGCAGGCGACACCTTAACC 780 770 780	LEU LYS ALA GLY LYS ASN LEU LYS ALA LYS T T A A A G C G G T A A A A C T T A A A A G C T A A G 790 800 810
VAL G T T (PHE VALUGIO	HR TICTA(YS AI A A G (
A A A C	THR PH ACTTT 880 . VAL	ASN GLU THR A A T G A A A C T P 740 GLN ALA C A A G C	ASN LEU LYS AACTTAAAAC 800 LEU ASP
: : :	THE 680 680 G	GLA GLA 740 740 C	EE 2008
	ALA G C A	ASN A A A	ASN A A (
	ALA G C C	LYS A A A A	LYS A A A
	ASP 3 A T 0	GLY G G C /	GLY G G T
	ASN P A A C G 670	ALA (3 C A G 730	ALA C 3 C G G 790
	ILE VTT/	ALA S C T C	LYS 1 A A C
	ALA ; C G ?	GLY 3 G T C	LEU 'TA?
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TGCTTCGACTTGACC

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GLY

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AACGGAAATGGTCAAAACGGTAATGTC...

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	GLY G G T 900	THR A C.A 960	
	ILE GLY ATTGG 90	LYS A A A	
	SER	ALA 3 C G	
	LEU TTG? 890	LEU 1 T G (
	LYS . A G T	LYS	
	860 AIA LYS VAL SER ASP LYS LEU SER ILE GLY G C G A A A G T G A T A A G T T G T C T A T T G G T G C C A A A G T G A G T A A G T T G T C T A T T G G T	ASP ILE THR SER GATATTACCAGT 920 ASP ALA ASN GLY LEU LYS LEU ALA LYS THR GATGCAAATGGCTTGAAATTGGCGAAAAC.A 950	
: :	. R . T . G	: : : ^Y .	:
SER.	8/U SER GAGT 880	SER A G T 930 I GLY T G G C	VAL
開 CCC	VAI A G T	THR ACCA ASP A A A A	ASIN
VAL TG?	LYS 3 A A	ILE TT71 ALA TGC	GLY
ASP A T G	860 ALA G C (ASP G A T P 920 ASP G A '	ASIN
T T G	× : : :	AL T T T T G 92 92 92 92 92 92 92 92 92 92 92 92 92	IIN
U U		. A .	٠.
ASF G A		LYS A A	G G
LYS A A A	0	ASN A A T O	ASIN
ALA 3 C G	820	THR 1	GLY
LEU PTA(LYS ASP THR ASN LYS VAL ASP ILE THR SER A A G A T A C G A A T A A G T T G A T A T T A C C A G T 910 ASP ALA ASN GLY G A T G C A A A T G G C	GLY ASN GLY ASN GLY GIN ASN GLY
ALA LEU ALA LYS ASP LEU ASP VAL THR SER GCTTTAGCGAAAGACCTTGATGTGACCTCT		LYS ASP THR ASN LYS VAL ASP ILE THR SER A A A G A T A A A G T T G A T A T T A C C A G T 910 930 ASP ALA ASN GLY G A T G C A A T G G C	GLY
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GATACCATTACAGGTATGACAACACAGCA... ALA :: GLN Œ GLY 開 ILE 瑶

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... A G C A A T G G C G T G C T G T G C A G A A T C A T A A T ASI N HIS WAL ALA Æ EX EX ASI SE

ALA ASP VAL LEU ASN ... CGTGCTGCGAGTGTGGCTGATGTAAAT... VAL SE ALA AIA

... ALA GLY TRP ASN ILE GLN GLY ASN

... GCAGGCTGGAATATTCAAGGCAACGGAGCG

ALA

GLY

强: ALA WAL 出

AGCGTTGATTTGTCAATGCTTACGACACA...

... GTAGATTTTGTCAATGGTACAAACACAAA ... VAL ASP PHE VAL ASN GLY THR ASN THR

VAL ASN VAL THR THR ASP THR ALA HIS LYS ...

GTGAACGTTACGACTGATACGGCTCACAAA...

... A A G A C A A C C G T C C G T G T G T A C A G G C M ... LYS THR THR VAL ARG

FIG.20F

				٠.	_				57	/20)4
			TYR	TAT	1320				E	CTC	1380
			LYS	AAG					CLU	GAG	
			ASI	AAT					GLY	0 G C	
			ASP	GAC	1310				ASN	AAT	1370
			VAL	G T G					CILU	GAA	•
			LYS	AAA					VAL	$_{\rm G}$ T $_{\rm C}$	
YT	TTCAATATGTTACGGAAGACGGC	1290	LYS THR VAL VAL LYS VAL ASP ASN LYS TYR	A A A A C C G T T G T G A A A G T G G A C A A T A A G T A T	8	.: dS	CTAAGCAAGACGGTTCGGCGGAT	1350	LYS	ATGGATAAAAAGTCGAAAATGGCGAGCTG 🔀	90
G G	5 C G		Æ	3 T T	1300	A.	9 9	, 	LYS	AAA	13
AS	A G A		出) ပ		A	0 0		\SP	AT	
GLU	G A		S	AA		SE	T C		T.	S S	
置	ACG	1280	LY	A A	:	GLY	G G T	1340	ME	A T	
VAL	G T T		•	,	•	ASP	GAC		•	•	
TYR	T A T					GIN	CAA				
GLN	CAA	0				LYS	AAG	0			
VAL	G T T	1270				ALA	GCT	1330			
LEU PRO VAL GIN TYR VAL THR GLU ASP GLY	TIGCCGG					TYR GLU ALA LYS GIN ASP GLY SER ALA ASP	TACGAAG				
PET I	TTG					TYR	TAC				

... A G C G G T C A A A A T C C G G T G A A A A T C A G C A A T II.E LYS VAL GCGAAAACCAAAGTGAAATTGGTGTCGGCA... 1410... GLN ASN GLY ... SER

GTTGCGGAAGGCACGGAAGAAACGATGCG... 1470... GLU ASN ASP ALA ... GIM GLY

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1370

1360

ALA ...

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LYS

THR LYS

ALA LYS

FIG.20H

GACACACTTTACGCCGAAAAGGT 1680 1680

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	58	/ 204	
GLN	ASP	ASP	?
C A A	G A C	G A C	
1500	1560	1620	
LEU	ALA	THR	. 271
TTG	G C C C	ACA	
ALA	ASP	SER	27.1
G C C	GATC	T C C	
LYS 1 A A A A 1490	ASN F A A C 1550	LYS 1 A A A A 1610	V.F. OV.F. OUR. CHE.
LEU TTG	GLY G G T 1	PHE T T T	Ē
GLN	GLY	LYS	£
C A A '	G G T	A A A	
VAL SER PHE LYS GIN LEU LYS ALA LEU GIN GTCAGCTTTAAGCAATTGAAAGCCAA GTCAGCTTTACAA 1480 1490 1500	GIU LYS GIN VAL THR LEU THR ALA SER ASN GAGAAACAGGTTACTTTAACTGCGAGCAAT 1510 1520 1530 ALA TYR ALA ASN GLY ASN ASP ALA ASP GCTTATGCCAATGGTGAACGATGCCGAC	GLY GLY LYS ALA THR GLN THR LEU ASN GGCGGCAAGTCAAACTTTAAACAAT 1570 1580 1590 GLY LEU ASN PHE LYS PHE LYS SER THR ASP GGTTTGAATTTAAATCCACAGAC GGTTTGAATTTAAATCCACAGAC	GLY GLU LEU LEU ASN ILE LYS VAL GLU ASN GGCGAGTTGTTGAACATCAAAGTAGAAAAT 1630 1640 1550

GGCGATAAAGTAACTTTGAAAGCCGGCGAG....1890

GLY

ALA

LYS

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WAL

ASP

1860

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ASN LEU LYS VAL LYS GIN ASP GLY THR ASN A A T C T G A A G G T C A A A G A C G G C A C A A A C A 1900 1900 1920	PHE THR TYR ALA LEU LYS ASP GLU LEU THR TTCACTTACGCGCTCAAAGATGAATTGACG 1930 1940 1950 GLY VAL LYS SER VAL GLU PHE LYS ASP THR GGCGTGAAGAGCGTGAGGTTTAAAGACACG	GLY SER ASN GLY ALA SER THR LYS 3 G T T C A A A G C A C G A A G 1990 2000 2010 1LE THR LYS ASP GLY LEU THR ILE THR SER A T T A C C A A G A C G C T G A C G T C G 2040	ALA ASN GLY ALA ASN GLY ALA ALA ALA THR GCAAACGGTGCGAATGGTGCGGCGGCGACT 2050 2060 2070
	PHE THR TYR A TCACTTACG 1930	ALA ASN GLY S CGAATGGTT 1990	ALA ASN GLY P CAAACGGTG 2050
	A F	& Ω □	Q D

... AAAGGTGCGGACAAGCAAACTCTGACTGTT

GCCGACAATACTGCCGCAACCGTGGGCGAT...

ALA

THR ALA

ALA ASP ASN

GLY

VAL

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THE

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LYS

GLY ALA ASP

··· LYS

GCCTATAAAGGCTTGACCAATTTGGATGAA...

ASP

ASN LEU

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GLY

LYS

TYR

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	GLY	5 G T 2160	LEU THR SER SER ACTGACCAGTTCC 2180 2190 ALA ASP ASN LEU THR LYS GIN TYR ASP ASP 250 GCCGACAACTTAACGAAACAATATGACGAT 2220 5220
	ASN VAL VAL SER GLY LEU LYS LYS PHE GLY	A A C G T T G T G A G C G G A C T G A A G A A T T T G G T 2150 2140 2160	ASP G A C
	LYS	A A A	TYR T A T
	LYS	, A A G 2150	GIN A'C A A 2210
	LEIJ C	ا ان ان	LYS A A A A
	GLY	₽ .5 .5	THR A C G
LYS A A 2130	SES C	2140	SER T C C 2190 AN LEU 1 C T T A 2200
AL I TTA	VAL	. G. T. G. 21	SER SGTT ASN ASN AAC
1. M. V. C. G.	VAL	ان تا تا	THR SCCA CCA ASP GAC
LYS 7	ASN .	A A	LEU 7 1 C T G A 2180 AIA G C C
ATA 213		: . :	PRO 1 C A C 218
GTA			ATC
ALA CGG	,	,	PHE T C A
GLY ILE SER ALA GLY ASN LYS ALA VAL LYS GGCATCAGTGCGGGTAATAAAGCGGTTAAA 2110 2130			ASP ALA ASN PHE ASN PRO LEU THR SER SER GATGCGAATTTCAATCCACTGACCAGTTCC 2170 2180 2190 ALA ASP ASN LEU GCCGACAACTTA
ILE ; TCA			C G A
LY 1 GCA			SP A ATG
ტ ტ			G B

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... AATGCCATTGCTTT

FIG.20L

		52/204	
ALA G C G 2340	GLU G A A 2400	ARG C G C 2460	ГУS
SER T C T	ASN A A T	ARG A G G (SER
ILE A T T	ALA G C C	GLY G G T	GLY
VAL ; G T C . 2330	ASN A A C 2390	ASN 2450	TYR
TRP TGG(ARG C G T 7	VAL G T C 2	GLY
GLY G G C	VAL G T G	THRACG	PHE
LEU TTG(S GLU G G A A 2370 ALA GIN VAL 5 C G C A A G T G 6	E HIS CCAT 2430 GLY LYS THR 3 GTAAAACG(GLU A A 2490 ALA
LEU ARG GLY LEU GLY TRP VAL ILE SER ALA T T G C G G C T G G G T C A T T T C T G C G 2330 2320 2340	LEU ASN LYS GLU C T C A A T A A G G A A 2360 TYR ASN ALA GLN VAL ARG ASN ALA ASN GLU T A C A A C G C G C A A G T G C G T A A C G C C A A T G A A T A C A A C G C G C A A G T G C G T A A C G C C A A T G A A T A C A A C G C G C A A G T G C G T A A C G C C A A T G A A T A C A A C G C G C A A G T G C G T A A C G C C A A T G A A 2400	ASN GLY ILE HIS A A C G G T A T C C A T 2420 VAL SER GLY LYS THR VAL ASN GLY ARG ARG G T T T C C G G T A A A A C G G T C A A C G C C 2460 2460	ASP GLU 5 A C G A A 2490
ARG C G C	ASN LY AATAA ASN CAACO	JY IL. SER	IS AS A A G A ALA
TTG(LEU AS A C T C A A 2360 T A C P	GLY ASN GLY 3 G C A A C G G T R 2420 VAL SER G T T T C	GLU LEU ALA LYS 3 A A T T G G C T A A A C 2480 ASN ALA
: : :	GLU LEU 3 A A C T C . 2360 TYE	ASP 2 A A 2420 G	AL/ 3 G C 2480
	GLU GA	G G (T T (
	C C C	SER AGCO	GLU GAA
	THR ACAG	LYS A A G 0	PHE TTT(
	THR 1 ACCA 2350	PHE I T T C A 2410	THR BACTT 2470
	ASP LYS THR THR GLY GLU LEU ASN LYS GLU 3 A C A A A C C A C A G G C G A A C T C A T A A G G A A 2350 2370 TYR ASN ALA GLN TYR ASN ALA GLN TA C A A C G C G C A A C G C G C A A	VAL LYS PHE LYS SER GLY ASN GLY ILE HIS 3 T G A A T T C A A G A G C G C A A C G T A T C C A T 2410 2430 VAL SER GLY LYS G T T C C G G T A A A A A A A A A A A A A A A A A	GLU ILE THR PHE GLU LEU ALA LYS ASP GLU: 3 A A A T T A C T T T G A A T T G G C T A A G A C G A A 2470 2480 2490
	ASP 3 A C <i>I</i>	VAL 3 T G	GLU 3 A A A

FIG.20M

	G G	T C T.	2580			ļ
	1.70	ACGGCAACGTTGTGAATGCGGAAAACT				
	11	GAA				
	A. I.A.	ရ ှိ ၁၅	2570			
		AAT	•			
	Į.	G T G				
: : :: :: ::	2550 AGN MAN (211 1.VS)	G T T	00.	:: B1	A A	2610
E G	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	A A C	2560	^හ	T C G	2
I.A A.	; ; ;	3 G G))	YR I	ACA	
AL A		A C) :	L NS	ACT	0
	2540	:		RO P	C G A	2600
	ت د د			SP I	A T C	
SP P	น น			ELY 7	$\mathfrak{g} \subset \mathfrak{g}$	-
RG 7	2530) 】	TCG	2590
E C	ر خ -			Į.	CAT	
ALA LEU ARG ASP ASN THR VAL ALA ILLE GLY	ب ر ر			GLY ALA PHE GLY ASP PRO ASN TYR ILE GLU	GGTGCATTCGGCGATCCGAACTACATCGAA	
~ (פ				G	

SER LYS ASN THR ... A A C G A T A A C C G T A T T A C T T C T A A A A A C A C T . . . THR ARG ASN ASP

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... GATAAAGCCGGTGGCAGCTACGCTTTCGGT

SES

GLY

GLY

LYS

ASP

... TTTGTGTTGGGTAATGGAGTTAATGCGAAA ... PHE VAL LEU GLY

GLY

TATAAAGCCAATGGAGATGTTGATACGGAA... GEY ASN TYR LYS

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... A C G G T A A A C G G C T T T G C C G G T G C A A C G G C G

... THR VAL ASN GLY

GGTAACACTACAACTGCTGGCACAACGGGT...

ALA

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ASIN

GLY THR THR GLY ...

ALA

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... A C C G T A A C C G T T A A G G A C A A A G A C G G T A A A ... GGGGCTACGGTTGAAACTCCGTTTATTG ... GGTAAAAACCTGAAATCTGATGGTACGGCG LYS VAL TYR LEU GLY SER THR VAL LYS ASP LYS GLU ASIN SER ALA LEU ... GAGACTACCGTTACTGTTCCTAAAGCGTTA... TAATAAATCGACTGCGACAAAAGATAAG.... 2830 2840 2850... ASP LYS ... ASN LEU THR VAL WAL ALA CLY LYS PRO LYS THR LYS GLY : 選 : M ALA W SER

FIG.20N

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3110

... A A T A A A G T G G C A A A C G T G C A G A T G C A G G T

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ACAGCAAGTGCATTAGCAGCTTCACAGTTA...

GLN LEU ...

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ALA

ALA

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ALA

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ALA

	ALA G C A 3000	ALA G C A 3060	GLY
	ALA G C G	TYR ALA VAL PATGCTGTGG	ALA
	VAL G T C	ALA G C T	ASP
	ASN 1 A A C 2990	TYR T A T 1050	ALA
	GLN C A A	LEU TTG	ARG
	ILE A T C	GLN CAG	LYS
HIS GLY ALA VAL SER VAL GLY ALA SER GLY CACGGTGCGTTTCTGTCGGCGAAGCGGC 2950 2970	GLU GLU ARG ARG ILE GIN ASN VAL ALA ALA GAAGAAGGTATCCAAAAGGTCGGGCA GAAGAAGGTATCCAAAAGGTGGGGAA 2980 3000	GLY GLU ILE SER ALA THR SER THR ASP ALA GGCGAAATTTCCGCCACTCCACGGATGCG 3030 3010 ILE ASN GLY SER GIN LEU TYR ALA VAL ALA ATTAACGGCAGCTGTGCTGTGCCA 3060	LYS GLY VAL THR ASN LEU ALA GLY GLN VAL A A A G G G T A A C A A T C T T G C T G G A C A A G T G 3070 3080 3090
SER AGC	J ARC A A G	ASP GAT GAT NGL)	GLN CAA
ALA 3 C A	J GLA AGA	THR ACC ASS TAA	GLY GGA ULY
GLY C G C C 2960	G A	SER TTCC. 3020 ILE	ALA 1 G C T 3080 ASP
WAL GTC	: : :	THR A C T 3 3	LEU CTT3
SER		ALA G C C	ASN A A T
VAL GTT 0	ı	SER T C C	THR ACA 0
ALA V G C G G 2950		ILE SATTT 3010	VAL G G T A A 3070
GLY G G T		GLU GAA	GLY GGGG
HIS C A C		0 0 C	LYS A A A

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TRP *** TGGTAATAGAATTCCGGATCCGC 3340 3350

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MET	3180	ARG C G A	3240		LYS A A A 3300	•
SER	I C A	SER TCA(GLY GGT/	
LYS	ช ช	GLY VAL 5 G G G T A T		٠.	GIN C A A C	
GLY	3170	GLY 3 G G	3230		SER 3290	
PRO	. C A .	ILE	3		ASN A A T ? 32	
SER MET	5	ALA G.C.T. 1			THR THR ACAACCI)	
SER		GLY G T 3210 LEU	0	ARG C G C 3270	THR ACA/	
ALA	CCACAAGCCICIAIGCCAGGIAAAICAAIG 3180 3170 3180	SER TYR GIN GLY AGTTATCAAGGT 3200 3210 GIN ASN GLY LEU ALA ILE GLY VAL SER ARG CAAAATGGTTTAGCTATCGGGGTATCACGA	3220	ILE AR	LEU SER GLY THR THR ASN SER GLN GLY LYS TTGTCAGGCACAACCAATAGCCAAGGTAAA 3280 3300	TYR GIN
GIN .	A A	R GL TCA TCA ASN		ILE IL TTAT	SER CA(TTT
PRO	ر لا	TYF A T A A A A A A		ILE 3 A T	EU TGT	GLN G G
<u>ا</u> :	رَّ : :	SER TY CAGTTA 3200 GIN	:	VAL G T C 3260	LEU	VAL G T 1
•	• •	ALA GLY SER SER 3 C G G G A A G T A G T T 3200 CLA CLA	•	GLY LYS VAL G G C A A A G T G A 3260		GLY G G T
		GLY G G A		G G C		ALA G C A
		ALA G C G 0		ASN A A T (ALA G C A
		ILE AATTG 3190		ASP P G A T A 3250		VAL G T T
	-	SER		ILE SER ATTTCC		THR GLY VAL ALA ALA GLY VAL GLY ACAGGCGTTGCAGCAGGTGTTGGTT
		VAL SER ILE ALA GLY SER SER TYR GIN GLY GTTTCTATTGCGGGAAGTAGTTATCAAGGT 3190 3200 3210 GIN ASN GLY LEU CAAAATGGTTTA		ILE SER ASP ASN GLY LYS VAL ILE ILE ARG A T T T C G A T A A T G G C A A A G T G A T A T T C G C 3250 3270		THR GLY VAL ALA ALA GLY VAL GLY TYR GLN A C A G G C G T T G C A G C A G G T G T T A C C A G

NTHi strain M4071 Hia

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TACAAACGGTTTGAAAGCTTATGGAAGT

GLY

TYR

ALA

ALA 3 C 60	ALA G C 120	SER A G 180
7 C	THR 7	2 8 8 8 9 15
TRP TGG(AC	THR
THR LCT'	ALA 3 C A 7	THR CG
I T A A	, 9 9	T A T
GLN C A 50	VAL G T 0	G G G
THR GIN ACTCAAP 50	THR VAL ACCGTGG 110	GLY GLY 3 G C G G T A 170
MET A T G A	ALA S C A A	THRACTO
	HR 0 SER	
VAL 3 T 30 VAL	THR A C SER C T C C	VAL G T 150 THR A A C T
S ILE PHE ASN VAL A A T T T T A A C G T 20 30 ILE TRP ASN VAL MET THR GLN THR TRP ALAT A T T T G G A A T G T T A T G A C T C C A A A C C C A A C C C C C C C	THR ARG ALA HIS THR OCTCGCGCCACAC 80 LYS ARG ALA SER ALA THR VAL ALA THR ALA CAAACGTGCCTCCGCAACCGTGGCAACCGC CAAACGTGCCTCCGCAACCGTGGCAACCGC	U SER THR THR VAL GTCTACAACAGT 140 1.50 GIN ALA THR THR GLY GLY THR THR SETTCAGGCGACACTACTGGCGGTACGACAAG
LYS ILE PHE A A A A T T T T A 20 ILE TRPT A T T T G G I	ALA H CCCA ARG CGTG	THR ACAA ALA GCG
TTT ILE	G B C G LYS	SER T
ILI 1 A T 20 20 1 A T	ARG CG 30 I) SE GTC 140 G
LYS A A A	THR ACT 8 	LEU S TTGT(140
MET ASN LYS ILE PHE ASN VAL GCGAATTCATATGAACAAATTTTAACGT 10 20 30 ILE TRP ASN VALTATTTGGAATGTT 40	VAL VAL SER GLU LEU THR ARG ALA HIS THR TGTCGTATCTGAACTCACTGCGCCCACAC 8090 LYS ARG ALA SERCAAACGTGCCTCCCAAACGTGCCTCCCAAACGTGCCTCC	VAL LEU ALA THR LEU LEU SER THR THR VAL CGTATTGGCGACGTTGTTGTCTACAACAGT 130 140 150 GLA ALA THR THR GLA ALA THR THRTCAGGCGACACT.
MET A T G A	GLU GAA	THR ACG1
A T 10	C T 70	ALA 130
T C	^Ω Ει	^დ ე
E	VAL 3 T A	LEU I T G
A	WAL TC	VAL T A 1
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O	C	O

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A G G T A A 240

...GAATAATCCGAATTTCAATGCTGC

ASIN

PHE ASP...

GIN

ALA ARG

LEG

TYR ASP

GLY ALA

CTCTGCAACTGATTTAGCTAGACAGTTTGA ...

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...TGGTGCTTATGACGGTTTATTAATCTAAA E

LEU VAL...

ASN LEU

TGAAAAAGATGCGAATAAAAATCTGTTGGT ...

...G A C T G A T G A T A A G G C G G C G A C C G T A G G C A A THR ASP ASP LYS

ASIN

GLY

TAAATTGGGTTGGGTATTGTCTAG...

...TAAAAACGGCACAAAGGAACGAGAAAGC

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GIN VAL LYS HIS ALA ASP GIJJ VAL LEJJ PHE A C A A G T C A T G A G T G T T G T T 450 GLJJ GLY LYS ASP GLY VAL THR VAL THR SER GLJJ GLY LYS ASP GLY VAL THR VAL THR SER T G A A G G C A A A G A C G T G T A C T T C 480	LYS SER GLU ASN GLY LYS HIS THR VAL THR CAAATCTGAAAACGGTAAACACCGTTAC 490 PHE THR LEU GLU LYS ASP LEU ASN VAL LYS TTTTACCCTTGAGAAGACCTTAATGTAAA 520 530
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69/204

GLY ALA ASN GLY ASN LYS VAL ASP ILE THR ...TGGTGCAAACGCCAATAAGTCGATATTAC 580 590 600 ALA LEU LYS GLY THR ASN ASP

AAACGCAACCGTTAGCGATAAATTA

VAL

ALA

ASIN

CAGTGATACAAACGGCTTGAAATTTGCGAA ... 610 620

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> TACGACAC 840

TGATTTTGTCAATACT 820 830

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VAL G T 660		-	
ASN A A T C	SER TCT	LEU TTG	
GLY 3 G T	LYS A A A '	VAL G T A C	
ASN A A C (THR ACAA	ASP 3 A T	,
GIN PAAAAA650	THR 1 CAA 710	ALA PSCTG	
E T C	GLY GTP	VAL	
PRO SER THR ASN GLY GIN ASN GLY ASN VAI ACCAAGTACGAATGGTCAAAACGGTAATGT 640 650	A SER THR LEU THR CCTCTACCTTAAC 680 680 ASP THR ILE THR GLY THR THR LYS SER ALPTGACACAATTACAGGTACAACAAATCTGC 720	L GIN ASN HIS ASN GCAGAATCATAA 740 ARG AIA SER VAL AIA ASP VAL LEU ASP TCGTGCTGAGTGTATTGAA 770 770	ALA
THR A C G 1 640	LEU T A A 69 11	HIS RATA 75 AIA AIA 760	GLY
SER AGTP	THR ACCT THR ACA	IN ASN HIS ASA GAATCATA? 751 ARG ALA ALA 16 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ASIN
PRO	ALA SER THR LESC CT 3 CCT CT A CCT 1 680 ASP THRT G A C A C A A A C A C A A A C A C A A A C A C A A A C A C A A A C A C A A A C A C A A A C A C A A A C A C A A A C A C A A C A C A A C A C A A C A C A A C C A C	ASP VAL GIN ATGTGCAGP 740 ARG	GLY ASN GLY ALA
 	ALA S C C T 680	VAL GGTGC 740T	GIN
	ILE	ASP 3 A T	TIE
	ASN GLY ACGGTA 670	VAL G T A (ASN
	ASN A A C (GLX 3 G T (TRP
	LEU LTA 2	ASN A A T (GLY
	HIS LEU ASN GLY ILE ALA SER THR LEU THR TCACTTAAACGGTATTGCCTCTACCTTAAC 670 680 690 ASP THR ILE THRTGACAATTACA	THR ASN GLY VAL ASP VAL GLN ASN HIS ASN A A C T A A T G T G T A G A T G T G C A G A T C A T A A 730 750 ARG ALA ALA SER ARG ALA ALA SERT C G T G C G A G T	ALA
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VAL ASP PHE VAL ASN GLY LEU ASN THR ASN AGTAGATTTTGTCAATGGTTTAAATACCAA 850 860 870	VAL ASN VAL THR THR ASP THR ALA HIS ASNTGTGAACGTTACGACTGATACGGCTCACAA 890 880 890	LYS LYS THR THR VAL ARG VAL ASP VAL THR CAAAAAGACAACGTCCGTGTGGATGTAAC 910 920 930 GLY LEU PRO VAL GIN TYR VAL THR GLU ASPGGGCTTGCCGGTCCAATATGTTACGGAAGA	JY ASIN GLU
7 LEU TTTAA 860	VAL TGTG	T G T G G 920 GLY G G G C	LYS VAL GLY
GLY F G G T 8		ARG 12 92 92 92 93 93 93 93 93 93 93 93 93 93 93 93 93	
ASN		VAL C G T C	VAL
VAL T G T (THR A C C	VAL
PHE T T T T 850		THR 3 A C A 910	THR
ASP AGA		LYS A A A (CLY GLU
VAL AGT,		LYS C A A D	GLY

71/204

ASP MET ASP LYS LYS VAL GLU ASN GLY LYS... GGATATGGATAAAAAGTCGAAAATGGCAA...

...GTATTACGAAGCCAAGCAAGACGGTTCGGC

GLY

ASP

GLN

TYR TYR GLU

TGTGAAAGTGGGCAATGA...

GGCGAAACCGT

72/204

- 4			
SER 1080	ASP G A 1140	SER A G 1200	SER . A G 1260
VAL GTAT	THR ACCO	ALA G C G	LEU TTA
LEU TTGG	ASN A A T	SER A G T	THR ACT1
LYS AAA7 0	R GLU G G A A 1130	LEU TTA	GIN C A A A
VAL L G T T A 1070	THR ACG 113	THR IACGT	ILE GATTC 1250
LYS A A A C	GLY G.G C	WAL	GLY 3 G A 7
LEU ALA LYS THR LYS VAL LYS LEU VAL SEI CTGGCGAAACTAAAGTTAAATTGGTATC 1060 1060 1080	O VAL LYS ILE SER GGTGAAAATCAG 1100 1110 ASN VAL ALA ASP GLY THR GLU ASN THR ASCAATGTTGCGACGGCACGGAAATACCGA 1120 1120	N LEU LYS ALA LEU 1 GTTGAAAGCCTT 1160 1170 GIN ASP LYS GIN VAL THR LEU SER ALA SEGCAAGACAGGTTACGTTAAGTGCGAG	"X GLX SER ASP ALA 1 C G T A G C G A T G C 1220 1220 1230 1240 1240 1250 1250 1250 1250
LYS A A A 1060	ILE SER 1 C A G 1110 ALA A G C G G 1120	ALA LEU 3 C C T T 1170 LYS GLN A A A C A G 1180	ASP P
ALA G C G I	AAA AAA VAL GTT(LYS PABABASPASP	SER AGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
LEU	VAL LYS STGAAAP) ASN VAL	LEU LITGA () GIN	GLY S GGTA (0 ASP
 	PRO V 1100 1100C 7	GIN L 2 A G T 7 1160 G C	GLY GI 3 G C G G 1220 C G
	D FE	9 9 9	T G G
	ASN A A T	LYS A A G	ASN A A T
	THR ACAP	PHE T T T	ALA G C C
	GLY G G T 1090	SER A G C 1150	TYR I A T 1
	ASN A A C	VAL G T C	ALA 3 C T 7
	ALA ASN GLY THR ASN PRO VAL LYS ILE SER GGCAAACGGTACAAATCCGGTGAAATCAG 1100 1110 ASN VAL ALA ASPCAATGTTGCGGAC	ALA VAL SER PHE LYS GIN LEU LYS ALA LEU TGCGGTCAGCTTTAAGCAGTTGAAAGCCTT 1150 1160 1170 GLA ASP LYS GINGCAAGACAGG	ASN ALA TYR ALA ASN GLY GLY SER ASP ALA C A A T G C T T A T G C C A A T G G C G G T A G C G A T G C 1210 1230 ASP GLY GLY LXS C G A C G C C A A G
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TTGGTTGAGGCTTCTGAATTGGT

... THR GLY

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SER

GLU ALA

GGCTACGATTCAAGACGGCGCAAAAAAACAAC...

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	GLU	G A	1320				LYS	AA	1380	
	ALA	GCA					GLY	GGT		
	ГХS	AAA					ASP	GAT		
	ILE	ATC	0.				ASP	GAT	0	
	ASIN	AAT	1310				GLY	ე ე	1370	
	<u> 1</u>	LTG,					VAL	3 T T (
ASN GLY LEU ASN PHE LYS PHE LYS SER THR	1280 ASP GLY GLU LEU LEU ASN ILE LYS ALA GLU	AGACGGCGAGTTGTTGAATATCAAAGCAGA	0	ASN ASP THR VAL THR PHE THR PRO LYS LYS	A A	1350	GIN	AGGTTCGGTGCAGGTTGGCGATGATGGTAA 🗭		ALA THR ILE GIN ASP GLY ALA LYS THR THR
SER I C C	GEU	GAO	1300	LYS	AAA	₩	WE.	GT (1360	THR
LYS A A A	GLY	0 9 9		PRO	0000		SE	TCG		LYS
PHE T T T	O ASP	A G A C		批	ACG	0	GLY	AGGT		ALA
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ASN A A T				VAL	3 T T					GIN
LEU	1270			THR	A C G (1330				ILE
GLY 3 G T'				ASP	3 A C i					扭
ASN GLY LEU ASN PHE LYS PHE LYS SER THR				ASN	AAATGACACGGTTACCTTTACGCCGAAAA		ě			ALA

73/204

ASP SER LEU ASN LYS LEU GLY TRP LYS VAL... TGACAGCCTGAACAAATTGGGTTGGAAAGT...

VAL.

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...GGGCACGGCACTGACGGCACAGGAGTGAC

VAL LYS...

ASP THR LEU

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CGATGGCACGCATACCGACACTTTAGTGAA...

...CACGGCGAATGGTGCAAACGGTGCAAGCAC

GLY ALA

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GLY ...GTCGGGCGATAAAGTAACTTGAAAGCCGG E THE

VAL

SER GLY ASP LYS

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1530 ...

GLY THR.... GACAATCTGAAGGTCAAACAAGAGGGTAC... 1590 ..

GEU

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ASIN

AIA THR ASN PHE

...AAACTTCACTTATGCGCTCAAAGATGAATT GE :

GLU PHE LYS ASP.... VAL 贸 VAL LYS

ASN GLY ALA ASN 1650 ... GACGGACGTGAAGAGCGTGGAGTTTAAAGA... 强

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LYS ILE THR LYS ASP GLY LEU THR ILE THR GAAGATTACCAAAGACGGCTTGACCATTAC		ASN THR ALA ASN THR ILE SER VAL THR LYS A A A C A C T G C A A C C A T T A G C G T A A C C A A 1750 ASP GLY ILE SER ALA GLY ASN LYS ALA VAL C A G A C G G C A T T A G C G G G T A A T A A A G C A G T 1800	

CTCAGCCGACAACTTAACGAAACAATATGA... GLN TYR ASP... E ASP ASIN

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LYS A A A	G A C 1950	ASN A A T	SER	2010 · · · · S 克克
TYR T A T 1900	PRO C G A 19	ASP G A C 1960	ILE V T T T	20 LYS
ALA G C C	THR	ALA G C T	VAL 3 T C A	ASP
ASN ALA TYR LYS GLY LEU THR ASN LEU CAATGCCTATAAAGGCTTGACCAATCTG	GIN C A A A	VAL ALA ASP ASN THR ALA ALA THR VAL CGTTGCTGACAATACCGCTGCAACCGTG 1960 1970 1	TRP r G G (2000 ALA ASP LYS THR LYS GLY GLU LEU ASN
: : :	GLU LYS SER LYS GLY LYS GLN THR PRO THR 3 A A A A A A G T A A A G C C A A C C C C C C C C C C C C	: : :	ASP LEU ARG GLY LEU GLY TRP VAL ILE SER	200
	GEN GGC		LEU	
	LYS A A A		G G C	
	SER A G T 1930		ARG C G C	1990
	LYS A A A		LEU TTG	
	GLU LYS SER LYS GLY LYS GLN THR PRO THR TGAAAAAGTAAAGGCAAGCAAACTCCGAC 1930 1940 1950		ASP LEU ARG GLY LEU GLY TRP VAL ILE SER	
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76/204

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TYR ALA...

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CATCGAAGATAAAGCCGGTGGCAGCTACGC ...

TTCGGCGATCCGAACTA 2270 2280

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SX1	' A A 2160	ALA 3 G C 2220	
AIA	T U	VAL G T G	
IR LEU ASP ASN GLY 2 A T T G G A T A A C G G 2120 THR ABG GII IIF THR PHF GIII LEI AIA LYS	TACGCGGAATTACTTTGAATTGGCTAA 2150 2140 2160	A PHE GLY SER GLY TTTCGGTTCTGG 2180 SER LYS ALA LEU ARG ASP ASN THR VAL ALA SER LYS ALA LEU ARG ASP ASN THR VAL ALA SER LYS ALA LEU ARG ASP ASN THR VAL ALA SER LYS ALA LEU ARG ASP ASN THR VAL ALA SER LYS ALA LEU ARG ASP ASN THR VAL ALA SER LYS ALA LEU ARG ASP ASN THR VAL ALA SER LYS ALA LEU ARG ASP ASN THR VAL ALA SER LYS ALA LEU ARG ASP ASN THR VAL ALA SER LYS ALA LEU ARG ASP ASN THR VAL ALA SER LYS ALA LEU ARG ASP ASN THR VAL ALA SER LYS ALA CA CG T G C C T T G C C C C T T G C C C A T A A C C C T T G C C C C A T A A C C C T T G C C C A T A A C C C T T G C C C A T A A C C C T T G C C C A T A A C C C T T G C C C A T A A C A C C T T G C C C A T A A C A C C T T G C C C A T A A C C C T T G C C C A T A A C C C T T G C C C A T A A C C C T T G C C C A T A A C C C T T G C C C A T A A C C C T T G C C C A T A A C C C T T G C C C A T A A C C C T T G C C C A T A A C C C T T G C C C A T A A C C C T T G C C C A T A A C C C T T G C C C A T A A C C C T T G C C C A T A A C C C T T G C C C A T A A C C C T T G C C C A T A A C C C T T G C C C A T A A C C C T T G C C C C T T G C C C A T A A C C C T T G C C C C C C C C C C C C C C	
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C	LTG 2150	SP A T A T A 2210	
PH	TTT 21	ASP G A T	
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GLY 3 G G 2130	¥ V	GLY G G 2190 A LEU C T T G	GLU G A 2250
ASN VAL SER GLY LYS THR LEU ASP ASN GLY CAATGTTCCGGTAAAACATTGGATAACGG 2110 2120 2130	G A A 2140	ASP GLU ASN ALA ILE ALA PHE GLY SER GLY AGACGAAATGCCATTGCTTTCGGTTCTGG 2170 2180 2190 SER LYS ALA LEUCTCAAAAGCCTTG	ILE GLY THR GLY ASN VAL VAL ASN ALA GLU A A T T G G T A C G G C A A C G T T G T G A A T G C G G G A A C G T T G T G A A T G C G G A 2230
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ASP G A 7		GLY GGG LY	ASIN A A
LEU T G	A C (ASP GLU ASN ALA ILE ALA PHE GLY A C G A A A T G C C A T T G C T T T C G G T T 2170 2170 SER LYS C T C A A A A	VAL T G
R I : A T 2120	. F.	A P T 2180	L V T G 2240
THR A C		ALA G C 2	G T
LYS A A		T T	ASIN A C
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G G		AIA G C	G G
SER C C 2110		ASN . A T 2170	THR C G 2230
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VAL 3 T 7		GLU 3 A 7	GLY 3 G 1
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ASI A A		ASI 3 A	III T
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ALA

...TTATCTCGGTAATGCTTCAACTGCGACAAA

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...CGGTGCGAAGACGAAAGTAACCGTGCCGCA

2440

VAL

SE

ASIN

VAL GLU

GLU

GLY

2490 .. GLY ASN

TYR. LEU

AGCCTTAGGCGAAACCGTAGAAATTCTGT ...

2460

LYS 2340 2400 ...TTTCGGTAACGATAACCGTATTACTAA ...TGCGAAACGTGATGCAAATGCAATGTACT <u>8</u> GLY ASIN THE VAL ARG LYS ALA SER VAL ASN... AAACACTTTTGTGTTGGGTAATAGTGTTAA ALA LYS ARG ASP GLY LYS ASP... GLY ALA LYS THR 2430 ... GLY ASN VAL VAL PEO TEO GEU LYS Mar. 2410 GLU

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GLY

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JIX G C	E C G C	SER THR CCAC 2700
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ALA G C	VAL G T	THR ACTT
THR ACT 0	SER I C T	ALA 3 C T
THR CAA	VAL T T 263(G ILE GIN ASN VAL 3 T A T C C A A A C G T 2660 2660 ALA ALA GLY GLU ILE SER ALA THR SER THF C C C G C A G G C G A A A T T T C G C T A C T C C A C 2680 2700
HR C T A	LA CGG	ILE .TTT
	T	I A A
GLY G 50 ASN A A (ALA C 10 GLY G G C	N VAL C G T 2670 HY GLU G C G A A 680
SP A T G 25 GLY 3 G T 2560	LY G T G 26 HIS C A C 2620	GLU GLU ARG ARG ILE GLN ASN VAL GAAGAAGGCTATCCAAAACGT 2650 2660 2670 MA ALA GLY GLUCGCGGCAGGCGAAA
I G	0 0 0 4	A A A A A A A A A A A A A A A A A A A
SER TC' AI AI 3 G C	ALA 3 C (GIN C A 1 AL AL
LYS A A A THR A C (HE TT THR ACG	TCO TALA ALA GCO
G A G A 2540T	C T C T 2600	ARG I) 260 260C G
C I	(15) S S S S S S S S S S S S S S S S S S S	ARC C G
ASN A A C	ASIN A A C	ARG 1 G A
A A A	AL TAA	GLU GLU ARG 3 A A G A A A G A O 2650
T A O	2 0	o o
GLY G G G 253	THR A C (259	GLU G A A C 2650
		SER GLY AAGTGGC
T T	9 9	SER C
AS G A	TH A C	SE A G
Ø	Ø	æ
	ASP LYS GLY LYS ASN LEU LYS SER ASP GLY AGATAAGGTAAAACCTGAAATCTGATGG 2530 2540 2550 THR ALA GLY ASN THR THR ALA GLY ALATACGGCGGTAACACTGCTGGCGC 2580	GLY LYS ASN LEU L'G G T A A A A A C C T G A A 2530 2530 THR VAL ASN GLY PR A C G G T A A A C G C T C C C C C C C C C C C C C C C C

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VAL

ASP ASN GLY LYS

ALA ILE GLY VAL...

GLY

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GLY

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2940

...A T C A A G A A T T T C C G A T A A T G G C A A A G T G A T

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GLY G G 2760		Or.
ALA G C T	ALA G C T	SER AGT
LEU	ALA 3 C G	SER A G T
ASIN A A C (LEU : T A (GLY G A A
THR A C A A 2750	ALA LE CATT 2810	A LA GI C G G C 2870
VAL ALA LYS GLY VAL THR ASN LEU ALA GLYTGTGGCAAAAGGGGTAACAAACCTTGCTGG 2740	JY LYS ARG ALA ASP S.C.A.A.A.C.G.T.G.C.A.G.A 2780 ALA GLY THR ALA SER ALA LEU ALA ALA SERT.G.C.A.G.C.A.A.G.T.C.C.A.T.T.A.G.C.G.C.T.T.C. 2820	## MET PRO GLY LYS 1 TATGCCAGGTAA 2840 2850 SER MET VAL SER ILE ALA GLY SER SER TYR ATCAATGGTTTCTATTGCGGGAAGTAGTTA 2860
ى ح	~	H A
GLY GGGG	ASP G A 2790 A ALA A G C A	LYS A A 2850 L SER T T C T 50
LYS A A A A 2740	JY LYS ARG ALA ASP S C A A A C G T G C A G A 2780 2790 ALA GLY THR ALA T G C A G G T A C A G C A A T G C A G G T A C A G C A A	G T A 28 28 VAL G T T 2860
ALA 3 C A	RG 7 G T G GLY GLY 3 G T	RO CAGCAG
ی ق	C A A	C C
VAJ I G T	LYS A A A A 10 ALA I G C	MET A T G 0 SEF A T C
	ASN LYS VAL GLY LYS ARG ALA ASP A T A A A G T G G C A A A C G T G C A G A 2770 2770 2780 ALA GLY THR ALAT G C A G G T A C A G C A 2800	SER M 1 C T A 3 2840A T
	VAL T G (ALA C C T
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	LYS A A	GIN C A J
	ASN A A T 2770	PRO C C A 2830
	GIN VAL ASN LYS VAL GLY LYS ARG ALA ASP A C A A G T G A A T A A A G T G G C A A A C G T G C A G A 2770 2780 2790 ALA GLY THR ALAT G C A G G T A C A G C A A C C A G C A C A C A C A C	GIN LEU PRO GIN ALA SER MET PRO GLY LYS A C A G T T A C C A C A G C C T C T A T G C C A G G T A A 2830 2850 SER MET VAL SERA T C A A T G C T T T C T
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	G A C	GLA C A
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81/204

TTGTCAGGCACAACCAATAGCCA... GLY ATTCGC

GLY LYS

...AGGTAAAACAGGCGTTGCAGCAGGTGTTGG ... 2990 3000

GLY

ALA ALA

TTACCAGTGGTAATAGAATTCCGGATCGC 3030 3030

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GTTTATGGCGATACGAATACTAAATTCAAT...

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ACGCAGTTGTCTGCAACGGCTGAAGCGAAC..

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ARG

FIG.22A

NTHi strain K9 hia sequence

		TRP ALA VAL	20 20 20 20 20 20 20 20 20 20 20 20 20 2				THR ALA VAL	CCGCCGTA	110
MET ASN LYS ILLE PHE ASN VAL ILLE TRP ASN	ATGAACAAATTTTAACGTTATTTGGAAT 10 30	VAL MET THR GIN THR TRP ALA VAL	40 40	GLU LEU THR ARG ALA HIS THR LYS ARG ALA	GAACTCACTCGCGCCCACACCAAACGTGCC	06	SER ALA THR VAL ALA THR ALA VAL	TCCGCAACCGTGGCGACCGCCGTA	100
ASN VAL	AACGTTA 20	:) : : : :	HIS THR	CACAC	80	:	T	:
出	ттт			ALA	CCC				
ILE	A A T T 10			ARG	C G C	20			
LYS	AAA	•		THR	ACT	•			
ASI	AAC	•		TEO	CTC				
MET	ATG			GLU	GAA				

82/204

LEU ALA TTGGCG

GIN ALA

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OIPN OIPN

... GLU LYS SER

... GAGAAAAGCCAACAAGTCAAACAGGCGGAT

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... G C A G C C A A T A A T T C A A T A G C A G A T T T A A A T ASS. 日日 ASP ALA ILE ASIN SER ALA ASIN ... ALA

FIG.22B

国 GLY ASP HIS VAL GLY ASP ASS. GLN

AAACAAAATGATGGTGTTCACGATGGTTTA...

ASN THR ALA ALA VAL ASP ASP E E

... TTAAATCTGAATGAAAACGGTGCGAATAAA

ASIN

ASIN

DET

ASIN

... LEU

ASI N

AAGCTGTTGGTGGATGACAATACTGCGGCG...

ASP GLY ... THR VAL

... A C C G T A G G C G A T T T A C G T A A A T T G G C T G G

GLU ASN ... GTCGTATCAACCAAAATGGCAAGGAAAT... GLY LYS ASIN LYS 璟 WAL



... A C A G G T A G T G C A A C A C A C C A A A A G T G A A T

VAL

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ALA

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... THR

TTAACGATTGGCGGTAGTACTACT... 550 570...

GATACC

VAL LEU PHE LYS GLY SER LYS GLY GLY GTGTTGTTTAAAGGCAGCAAGGCGGT 430 440 450	GTGCAGGTTACTTCCACTCGAAAACGGC GTGCAGGTTACTTCCACCTCTGAAAACGGC 470 480	HIS ALA ILE THR PHE ALA LEU ALA LYS CACGCCATTACCTTTAGCGAAA 490 510 ASP LEU ASP MET ARG THR ALA THR VAL SER PRGACCTTGATATGAGAACTGCGACTGTGAGTZ 540 PS	THR LEU THR ILE GLY GLY SER THR THR
GLU VAL I GAAGTGT		LYS HIS PAAACACG	强
GIA G A		LYS. A A	ASP

GTGACTAGCACGGCAAGCGGCTTGAACTT... E GEY Ŗ AIA 置 VAL THR

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GTTCAAGATGTTTTAAATAGTGGTTGGAAT...
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GLN ASP VAL

FIG.22D

	. 057.	204
ASP . G A T 660	GLY GGGG 720	SER A G C 780
G G C	ASN THR GLY AATACTGG(ALA ALA SER SCGCAAGO
ASN A A T	ASN A A T	ALA G C G
ALA G C T 7 650	LEU T T G	ARG C G T 770
GLY 3 G T (LEU	LYS A A A
THR	THR 1 C T (LYS A A A A
ALA LYS GLY ALA THR GLY ALA ASN GLY ASP G C G A A G G C G C T A C G G C G A T G G G C G A T G G G C G A T G G G C G A T G G G C G A T G G G C G A T G G G C G A T G G G C G A T G G G C G C A T G	THR VAL HIS LEU THR ASN ILE ALA SER ACTACGGTTCACTTGACTATTGCTTCA 670 680 690 THR LEU GIN ASP THR LEU LEU ALY ASP THR ASP THR ASP THR 1.00 ASS TACTGGG	VAL VAL SER LYS LEU ASP GLY ASN GLY ILE G T T G T G G T A T G G T A T T 730 740 THR ALA ASP GLU LYS LYS ARG ALA ALA SER A C T G C T G A G A A A A A A C G T G C G G C A A G C 760
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85/204

AAAGACACAAATCAAGTCGCAAGTAAT... 1030 1030 1040 1050...

ASN ASN ...

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ALA

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GLN

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ASP

	86/204	
GLU G A A 900	ILE A T.C 960	ASN A A T 1020
SER AGT(VAL LYS	LYS ALA
GLY GGAP	VAL	LYS A A A
LEUSER TGAGCG 890	THR LYS CTAAAG 950	THR GLY CTGGA1
LEU	THR	THR
PHETT	SER	PHETT
SER ASP ASN VAL ASP PHE VAL ARG THR TYR TCTGATAACGTTGATTTTGTCCGTACTTAC 850 870 ASP THR VAL GLU PHE LEU SER GLY SER GLU GACACAGTTGAGTTTTTGAGCGGAAGTGAA 900	GLU THR THR LEU VAL THR VAL ASP SER GLU GAAACTACACTGGTTACAGTGGATAGTGAA 910 920 930 SER ASN GLY LYS SER THR LYS VAL LYS ILE AGTAATGGAAAATCTAAAAGTTAAAATC 950	GLY ALA LYS THR SER VAL ILE LYS GLU LYS GGTGCGAAGACCTCTGTTATCAAAGAAA 970 970 ASP GLY LYS LEU PHE THR GLY LYS ALA ASN GACGGTAAGTTATTACTGGAAAAGCTAAT 1000 1020
THR ACT	SER (A G T G T G B A T G G A T G G A	GLU GAA ZY LY
VAL ARG STCCGTP S60 ASP THR GACAC	VAL ASP 3 T G G A T P 320 SER ASN . A G T A A '	LYS AAAASP GI
VAL ARC FGTCCG 860 ASP	VAL G T G 920 SE	L ILE LYS GLU TATCAAAGA 980 ASP GLY GACGGTA
PHE	THR A C A C	UAU G T T P
ASP G A T 3	VAL	SER TCT
ASN VAL ACGTTC 850	тнк гал САСТG(910	LYS THR AGACCT 970
ASN A A C 8	THR A C A 9	LYS A A G
ASP G A T	THRACT	GLY ALA
SER T C T (GLU GAA	G G T

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> ... VAL THR GLY ASP ALA THR ASN GLY ILE THR ... GTAACTGGCGATGCTACCAATGGTATTA.CT

GLY THR THR ALA VAL ...

TTTGCTGATGGCAATGGTACAACTGCAGTC..

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ALA ALA ASP ASP THR ASP GLU GLY LYS GLY G C A G C T G A T G A T G A T G A G G G C A A A G G C G C A G C T G A T G A T G A T G A G G C A A A G G C	LEU VAL THR ALA GLU THR VAL ILE ASN ALA TTAGTCACTGCAGAGACTGTTATCAATGCA 1090 1100 VAL ASN LYS ALA GLY TRP ARG ILE LYS THR GTAAACAAGGCTGGTTGGAGAATTAAAACA 1120 1120		GLU THR VAL THR SER GLY THR ASN VAL THR GAAACTGTCACATCAGGCACAAATGTAACC 1180 1190 1200
	LEU TTA(THR ACGG	

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	YS ILE THR AAATCACT 1320	LA THR ASN CAACCAAT 1380	
	ASN ASP GIN LA A A C G A C C A A A 1310	ALA PRO ASP A GCCCCTGATG 1370	
VAL LYS TYR GIU ALA LYS VAL GLY ASP GLY GTTAAATACGAAGCGAAAGTTGGCGACGGC 1270 1280 1290	EU LYS ILE TGAAGAT	ALA ASP THR THR ALA LEU THR VAL THR GLY GCAGATACGACCGCACTTACTGTGACGGGC 1330 1340 1350 GLY LYS VAL THR ALA PRO ASP ALA THR ASN GGTAAAGTTACTGCCCTGATGCAACCAAT 1380	GLY LYS LYS LEU VAL ASN ALA SER GLY LEU GGTAAGAAACTTGTTAATGCAAGTGGTTTA

88/204

... GCTGATGCGTTAAACAAATTAAGTTGGACT 国 ASIN 1410... 国 ALA ASP ... ALA

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GCAAAAGCTGAAGCAGATACTGCTAATGGC.. ASIN ALA ASP ALA GE LYS ALA

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TTAGGTACAGGAAATAATGGTGCGAAAACT... GLY ALA LYS THR ... ASN ASIN GLY

GLY ASP ASN LYS H CIT

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THR VAL GE GLY ALA LYS

THR PRE : GAAGTTAAAGCAGGCGAAACGGTAACCTTT..

... LYS ALA GLY LYS

... A A A G C G G C A A G A A C T T A A A A G T G A A A C A A

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TTTACTTATTCACTGCAA... SE TYR 開 GGTGCGAAC ASIN ALA

... ASP

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FIG. 22J

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ASP G A C 1920	LYS A A A 1980	LYS A A A 2040	ILE A T T 2100
ALA G C C (ASP G A C	VAL G T G	GLU GAA1
THR VAL ACTGTTC 910	ALA G C G	ASN GLU AATGAA 330	ARG C G T
THR G A C T 1910	3 SER TTCT(ASN : A A T 2030	ARG 7 A G G (2090
LEU CTG	ILE ATT 1	ALA 3 C C 7	ASN GLY ARG ACGGTAGC
THR ACT	VAL G T C	ASN A A C G	ASN A A C (
ALA ASP LYS GIN THR LEU THR VAL ALA ASP G C G G A C A A C T C T G A C T G C G A C A C 1910 1920	ASN THR ALA ALA THR VAL GLY ASP LEU ARG A A T A C T G C C C A A C C G T G G C G A T T T G C G C 1930 1940 1950 GLY LEU GLY TRP VAL ILE SER ALA ASP LYS G C T T G G C T G G G T C A T T T C T G C G A C A A A 1980	THR THR GLY GLU LEU ASP LYS GLU TYR ASN A C C A C A G G A A T A C A A C 1990 2000 2010 ALA GLN VAL ARG ASN ALA ASN GLU VAL LYS G C G C A A G T G C G T A A C G C C A A T G A A G T G A A A 2010	LYS SER GLY ASN GLY ILE ASN VAL SER A A A A G C G C A A C G G T A T C A T G T T T C C 2050 2060 2070 GLY LYS THR VAL G G T A A A A C T G T C A 2080
	ASN A A T	THR A C C	PHE TTC2

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GGTAAACCGAAAGT

VAL

LYS

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GLY

ALA

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... AATGCCAACGACAAAGTCCGTTTTGCTAAT ... 2520

ASN ASP

... ASN ALA

GCCTTGTCTGATAAATTGGAAACCGTA..

THR VAL ..

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... GGCGATAAATGGTATTACACGAAAGATGAC

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AAACGGTAAGAAAATCGTTAAAAT...

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) -	A A A 2580	THR A C.C 2640	
o C	G A T	ASN A A T	
> خ	2 g g	TYR T A C	
NO A	A A A C 2570	ILE A A T C 2630	
414	G C A	GLN C A A	
d D d	GAT	THRACGO	
ASN THR LYS VAL SER ALA ALA THR A A T A C C A A G T G A G C G G C A A C G 2530 2530 2540 2550	GTGGAAGCATCGATGCAAACGGCGATAAA	THR THR PHE VAL LYS THR ASP VAL A C A A C C T T T G T G A A A A C C G A T G T G 2590 2600 2610 CLU LEU PRO LEU THR GLN ILE TYR ASN THR	ASIN
ALA G C A	A A G	ASP 3 A T (1 PRC G C C	LYS
ALA 3 C G	GGA	THR ACCO LEU	VAL
SER 3 A G C (2540	р П	G A A A A 2600 GLU	ASN GLY LYS LYS ILE VAL LYS ASN
VAL GTG	• • •	VAL GTG 2	LYS
LYS A A A		PHE T T T	LYS
THR ACC 0		THR ACC 0	GLY
ASN 7 A A T A 2530		THR T ACAA 2590	ASIN
		THR ACT,	ALA
GLY LEU G G T T T A		VAL THR GTGACT	ASP P

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A A A 2760		THR A C A	2820			PR 8	CCA	2880
GCAAGAAA 2760		LYS				ASP	GAT	
၁ ၅ ၅		ASP G A T	! !			E	C T T	
G A C 2750		THR A C G	2810			SER	AGC	2870
T C A		SER	7			VAL	GTC	2
G A T		GLY G G T				VAL	GTT	
CTTGGCAATGTGGATTCAGACGGCAAGAAA 2740 2750 2760	VAL VAL LYS GLU ASP ASN LYS TRP TYR HIS GTTGTGAAGGACAACAAGTGGTATCAC 2770 2780 2790	VAL LYS SER ASP GLY SER THR ASP LYS THR	2800	GIN VAL VAL GLU GLU ALA LYS VAL SER THR	CAGGTGTCGAAGAAGTAAAGTTCTACC 2830 2840 2850	ASP GLU LYS HIS VAL VAL SER LEU ASP	GATGAAAACACGTTGTCAGCCTTGATCCA	2860
	VAL GTTG			GIN	C A G			

A A T G A T C A A T C A A A A G G T A A A G G C G T G G T C... VAL VAL .. GLY GLY LYS LYS SE GLN ASP ASIN

... A T T A A C A A T A T G G C T A A T G G C G A A A T T T C T II. GET) ALA ASIN GLY ASN MET ... ILE ASIN

A A A T C A A T G G T T T C T A T T G C G G G A A G T A G T . . .

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FIG.220

				90/204		
		THR A C A 3000		ALA G C A 3060		GLY G G T 3120
		VAL G T A		ARG C G T		PRO C C A
		GLY GGG		LYS A A A		MET A T G
		LYS A A A A 2990		GLY G G C 050		THR 3110
		ALA G C A		WAL G T G		ALA 3 C C 3
		VAL 3 T G		LYS A A A (GIN
ALA THR SER THR ASP ALA ILE ASN GLY SER	GCCACTTCCACCGATGCGATTAACGGAAGT 2950 2970	GIN LEU TYR ALA VAL ALA LYS GLY VAL THR CAGTTGTATGCCGTGGCAAAAGGGGTAACA 2980 2990 3000	ASN LEU ALA GLY GIN VAL ASN ASN LEU GLU A A C C T T G C T G G A C A A G T G A A T A A T C T T G A G 3010 3030	GGCAAAGTGAATAAAGTGGCAAACGTGCA 3040 3050 5	ASP ALA GLY THR ALA SER ALA LEU ALA ALA GATGCAGGTACTGCAAGTGCATTAGCGGCT 3070 3080 3090	SER GIN LEU PRO GIN ALA THR MET PRO GLY TCACAGTTACCACAAGCACTATGCCAGGT 3120

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TYR GIN GLY GIN ASN GLY LEU ALA ILE GLY TATCAAGGTCAAATGGTTTAGCTATCGGG 3180	VAL SER ARG ILE SER ASP ASN GLY LYS VAL G T A T C A A G A T T T C C G A T A A T G G C A A A G T G 3190 ILE ILE ARG LEU SER GLY THR THR ASN SER A T T A T T C G C T T G T C A G C C A C A A T A G T 3220 3230	GIN GLY LYS THR GLY VAL ALA ALA GLY VAL CAAGGTAAAACAGGCGTTGCAGCAGGTGTT 3250 3250 GLY TYR GIN TRP *** GGTTACCAGTGGTAATAGAATTCCGGATCC 3300

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TGGAATGTTGTGACTCAAACTTGGGT

...CACCAAATG

GCGTTGTCTGCAAC SER ALA E

...GGCTGAAGGAACAACAATACTTCTGTTACGAA

NTHi strain K22 Hia

ASIN

GCGAATTCATATGAACAAAATTTTAA... I.YS II.E

...CGTTATT

THR ARG ALA HIS... E D E C

TGTCGTATCTGAACTCACTCGCGCCCA

CGTATTGGCAACT

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ASP

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... THR ALA ALA THR VAL GLY ASN LEU ARG LYS LEU ...TACCGCCGCAACCGTAGGCAATTTGCGTAAATT

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		SER	100	230				CLU	BAA	290			
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		泯	000	220				ASIN	ATC	280			
A A	:	THR	CAA	٠	LYS	A A	:	LEGI	TAA		ASIN	A A	:
V.C.T.		ASIN	ATA		TYR	FAT		DET.	TAT		ASP	BAC	
JAT	_	肥	TTA	210	ALA	CT	_	GLY.	GCT	270	ALA	C C (_
AATGCTTATGGCGATACTAA	200	PHE ASN THR 1THR ASN ASN SER ILLE ALA ASP LEU	TTTTAATACAACCAATAATTCGATAGCAGATTT	.:	HIS VAL GIN ASP ALA TYR LYS	CACGTTCAAGATGCTTATAA	260	:	AGGCTTATTAAATCTGAATGAAAAAGATACAAA 改	2	SER PHE LEU VAL ALA ASP ASN	AGTTTCTTGGTTGCCGACAA	320
l A T (UIS	A A					DET T	TG	
CHI					VAL	TI:					铝	TCI	
ATC	190				HIS	BCC	250				SES	GTJ	310
TG						AAC					SER	CAP	
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LYS A A A	LYS AAAC THR	
VAL G T A	SER TCTP LYS	
GLN C A A	SER SER SER FCCAGCTCTP 470 GLU VAL LYS 3 A G G T A A A A B	
TYR G TATC 410	SER 2 TCCA 470 GU V GAGG	
THR ARG ASN GIJU LYS SER TYR GIN VAL LYS GIN CACAAGGAACGAGAAAAGCTATCAAGTAAACA 390 400 400 420	PHE THR GLY SER TTACTGGATC 440	
LYS A A A	VAL GITA PHE TITG	
GLU G A G 400	GLY SER G G A T C ALA ALA THR G C T G C A A C G (460 SER VAL T C T G T T C T G T LYS GLY SER A A A G G T A G T C	:
ASN A A C	SER. TC. ALA GCA GT. GT.	ALA
THR ARG ASN GLU CAAGGAACGAGA	GIU VAL LEU PHE THR GLY SER G A A G T T C T T T A C T G A T C 430 GLY ALA ALA THR T G G T G C T G C A C G (C A A C G C A C C A C C C A C C C A C C C A C C C A C C C A C C C A C C C A C C C A C C C A C C C A C C C A C C C A C C C C A C	ASIN
THR A C A 390	THR TACT 440 GLY TGGT (450 R ILE CATT 500 THR TACC?	GIN VAL
: : :	HE TH 440 GLAT G G 450 THR IL A C C A T 500 TA CT A C	GIN
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		THR VAL LYS ASP VAL ALA LYS ALA ILE ASN ASP	AACTGTAAAAGATGTTGCTAAGGCGATTAACGA	650				THR ASP ASP ILE GLU ASN GLY ALA ALA GLY 🥃	ATG	690 700 710 720 9				呂
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LYS	A A G	:	Α	630	LYS	AAA	9	:	: :	690	ASP	GAC	7	:
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GLY ALA	TGGAGCT				AIA AIA	TGCCGCA				•	LYS ASIN	CAAAAAT		
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...CAAAGCAGGGGACTTAAAAGCGGGG. ... 750 770 780 780 LYS LEU ASP GLN. TAAAAACTTAAAAGCTAAGTTAGACCA ALA LEU LYS ASIN

TTGACCGATACCATTAC

TGGTCAAACGGTAATGTCCACTTAAA 980

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LYS A A 840	ASN A A 900	ASN A A 960
THR PHE ALA LEU ALA LYS ACCTTGCTTTAGCGAA 830 840	ILE GLY LYS ASP THR LTTGGTAAAGATACG 890	GLY G G A
TAG.	ASP A T A	ASN A C
4 H	IS I	LY G T A
T G C B30	(L) T A 1 890	R G A G 950
PHE T T	GEN G G	TH
THR ACC	ILE A T I	LYS A A I
ASN GLY LYS SER VAL THR PHE ALA LEU ALA LYS AAATGGTAAATCAGTAACCTTTGCTTTAGCGAA 810 820 820 830	SER ALA LYS VAL ICTGCGAAAGT 860 SER ASP LYS LEU SER HE GLY LYS ASP THR ASNGAGTGATAAGTTGTCTATTGGTAAAGATACGAAGAGTGATAAGTTGTCTATTGGTAAAGATACGAAB70	SER ASP ALA ASN AGTGATGCAAA 920GLY LEU LYS LEU ALA LYS THR GLY ASN GLY ASNTGGCTTGAAATTGGCGAAAACAGGTAACGGAAATGGCTTGAAATTGGCGAAAACAGGTAACGGAAATGGCTTGAAATTGGCGAAAACAGGTAACGGAAATGGCTTGAAATTGGCGAAAACAGGTAACGGAAA
C A G 820	起 T G 7 880	T G (
SS	AL T T KS I	A
T A P	S V A G	A A B B B B B B B B B B B B B B B B B B
G G	LY G A B ASI G A	TG C
ASN AAT 810	SER ALA I C T G C G B 860 SER G A G T G	ASF 2 G A 220 G G G 930
	SER TCT 8	SER AGT 92,
	ASP VAL THR SER ALA LYS VAL GATGTGACCTCTGCGAAAGT 850 860 SER ASP LYS IGAGTGATAAGT	ASP ILE THR SER ASP ALA ASN ATATTACCAGTGATGCAAA 910 CLY LEU LYS LTGGCTTGAAAT
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LYS AL A A A G C 1870		ASP GI 3 A T G P 1930	ALA SE SCAAG 1990
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LEU TTG	ALA G C A	ASP 3 A T	LYS A A A A
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LYS 7 A A G 2510	SER G	GLY 7 5 G T A 2630	LYS T A A T 2690
SER LYS CCAAAA(251(LYS AAA 1	PHE TC0	ALA LYS TYR ; C G A A A T A T 1
ALA PHE CLY TYR CLY SER LYS ALA LEU ARG ASI TGCTTTCGGTTATGGCTCAAAAGCCTTGCGCGA 2490 2500 2520	GLY THR GLY ASN 3 G T A C G G C C A A 2540 VAL VAL ASN ALA GLU LYS SER GLY ALA PHE GLY C G T G T G A A T G C G G A A A A T C T G G T G C A T T C G G 2550 2580	GLU ASP LYS ALA 3 A A G A T A A A G C 2600 GLY GLY SER TYR ALA PHE GLY ASN ASP ASN ARCCGGTGGCAGCTACGCTTTCGGTAACGATAACG 2640 2620 2640	THR PHE VAL LEU ACTTTTGTGTT 2660 CLY ASN CLY VAL ASN ALA LYS TYR LYS ALA ASNGGGTAATGGAGTTAATGCGAAATATAAAGCCAAGGGTAATGGAGTTAATGCGAAATATAAAGCCAA
TYR F A T C 2500	ALA 3 C G G 2560	ALA G C SER TYR A G C T A C G	VAL 3 T T A
GLY 3 G T 3	ASN A A ASN AI A A T G C	ASP LYS ALA 3 A T A A A G C 0 GLY GLY SER T GT G G C A G C T 10	FHE VAL LEU TTGTGTT ELY ASN GLY VAL GTAATGGAGTT7
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ゴ張 A C C	LYS A A A
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GLU GAG	GLY G G T
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GLY ALA THR ALA HIS GLY GGTGCAACGCGCACGGTG 2920	ALA ALA GLY GLU ILE 3 C G C A G G C G A A A T 7 2990	VAL STGG	ALA GLY 3 C A G G T 7
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	SER VAL TTCTGTC	ALA THR CGCCACT	ASN LEU AAATCTT

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LEU ALA ALA SER GIN LEU PRO GIN ALA ATTAGCAGCTTCACAGTTACCACAAGC 3130 SER MET PRO GLY LYS SER MET VAL SER ILE ALA CTCTATGCCAGGTAATCATGGTTTCTATTGC 3150 3150 3150	GLY SER SER TYR GIN GLY GIN ASN GLY GGGAAGTAGTTATCAAGGTCAAAATGG 3190 ISU ALA ILE GLY VAL SER ARG ILE SER ASP ASN IEU ALA ILE GLY VAL SER ARG ILE SER ASP ASN TTTAGCTATCGGGGTATCACGAATTTCCGATAA 3210 3210	GLY LYS VAL ILE ILE ARG LEU SER GLY TGGCAAAGTGATTATTCGCTTGTCAGG 3250 THR THR ASN SER GIN GLY LYS THR GLY VAL ALACACAACCAATAGCCAAGGTAAAACAGGCGTTGC3270 3280 3380	ALA GLY VAL GLY TYR GLN TRP *** AGCAGGTGTTACCAGTGGTAATA 3310 3320
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THR A C G 230	VAL G T A (THR ACC 350	ALA
GLY 3 G C	LYS GLY	SER AGCA	VAL
GLU 3 A A (LYS A A A A	GLN C A A	SEE
HIS SER ASP LYS GLU GLY THR GLY GLU LYS CATTCCGATAAAGAAGGCACGGGAAAAAA 220 230 240	GLU VAL THR GLU ASN SER ASN TRP GLY ILE GAAGTTACAGAAATTCAAATTGGGGAATA 250 270 TYR PHE HIS ASN LYS GLY VAL LEU LYS ALA TYR PHE HIS ASN LYS GLY VAL LEU LYS ALA TATTTCCACAATAAAGGAGTACTAAAAGCC 300	GLY ALA ILE THR LEU LYS ALA GLY ASP ASN GGAGCAATCACCCTCAAAGCCGGCGACAAC 310 320 310 LEU LYS ILE LYS GIN SER THR ASN ALA SER CTGAAAATCAAACAAAGCACCAATGCCAGT 350	SER PHE THR TYR SER LEU LYS LYS ASP LEU AGCTTCACCTACTCGCTGAAAAAAGACCTC 370 370 THR ASP 1F11 THR SER VAL ALA THR

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ASN ALA GLY TRP ASN ILE LYS GLY ALA LYS A A T G C A G G T T G G A C A T T A A A G G T G C T A A A 640 650 650	L ASP TGAT 690 SER ALA TYR ASN ASN VAL GLU PHE TCCGCTTATAATATGTTGAATTT 700	THR LEU ASP VAL A C G C T T G A T G T T 740 VAL LEU THR ALA LYS GLU ASN GLY LYS THR G T A T T A A C A G C T A A A G A A A A C G G T A A A A C A 770	PRO LXS THR SER C C G A A A A C C T C T 810 800 810 VAL ILE LYS ASP GLY LYS PHE G T T A T C A A G A A A A A A G A C G G T A A G T T A T T T 820 840
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GLY GGT	VAL G T T	GLY G G T	LYS AAG1
LYS A A A C 650	ASN A A T (ASN A A C 770	ASP GLY ACGGT 830
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ASN AAC1	TYR T A T	LYS A A A A	LYS . A A A (
TRP T G G 1 0	ASP 3 A T 690 R ALA C G C T 7	ASP VAL 3 A T G T T 750 U THR ALA A A C A G C T	THR SER A A C C T C T 810 ILE LYS GLU T C A A G A A B
GLY 7 3 G T T 640	ASP TGAT 690 SER P	VAL TGTT 750 THR A	SER . 1 C T . 810.
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THR ACC 5	PHE TTT	GLY G G T 5	GLY
ILE VAL ALA ASP THR THR VAL LEU THR VAL A T C G T T G C A G A C A C G T A C T T A C T G T G 5260 5270 5280	ALA PRO ASN ASN G C T C C G A A T A A T 5300 5310 GLY ASP GLY LYS LYS PHE VAL ASP ALA SER G G C G A T G G T A A G A A A T T T G T T G A T G C A A G T 5320 5330 5340	N LYS LEU SER TAAATTAAGC 5370 TRP THR ALA THR ALA GLY LYS GLU GLY THR T GGACGCAACTGCTGGTAAAGAAGGCACT	ALA
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C G T	; C C G	AAGTC	PATGTAACAC
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FIG.24G'

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LEU	ALA	SER	SER
CTT	G C A (T C A	T C A
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GLU GAAO 0	GIN C A G 270 t GLY A G G C P	ALA	C G		340	ARG 390 GLU
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VAL G T G	HIS GI CACGI LIXS AAAA	GLU A	AAA		. A .	U ALA GLU GGCAGAA(TVR SER VAL
ILE A T T	LEU HE TTACA 260 ALA	e cer	TTAG 320		ر. A	LEU A TGG 180
: : :	LEU 1 T T T 260 260 6		C T T 320	: :		л <u>ге</u> АСТ 380
	PHE T T T	TYR	T A			GLU G A A
	GIN C A A '	LYS	GATAAAAATACTTAGAAAATGCG 320 330			ASN GIN THR GLU LEU ALA GLU ARG A A T C A A C T G A A C T G G C A G A A C G T 370 380 380 AN SER VAL GIA
	ALA ALA GIN CCGCCCA P 250	ГХS	A A A .0			T C A A 370
	ALA 13 C C G 250	ASP	G A T A 310			ASN A A T (370
	CYS I G C (PHE	T T T			GLN C A A
	ILE CYS ALA ALA GIN PHE LEU HIS GLU GLN ATCTGCGCCGCCAATTTTTACACGAACAG 250 270 ALA LYS THR GLYGCAAAAGGCA	CLY	GGTTTT			GLU GLN GAACAA

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ARG C G T 480	GLY LEU GGTCTT 540	ASN A A T 600		
LEU CTG	GLY	VAL G T T		
GLU G A A	PHETTT	MET A T G		
LEU TTA(HIS CAC 530	ASP G A T 590	-	
TYR A T '	PRO C C G (SER I C A		
ASP 3 A T T	ALA 3 C A (R G TO LYS TYR A A A T A T '		
J A 50 SER A G C G	HE T.T 510 LEU T.T.A.G	 	:	
GLU GAA 450 U SER AAG C (PHE 510 0 LEU LEU 520	SER T C G 570 G LYS C A A 580	LYS	A A A 630
TATTC TATTC TE GIU	A GLU CGAAT SER GLU	GACAT ILE ARG	ALA	GCA
ASP GATI	ALA 3 C C (5 SEF A T C	TRP I G G) ILL C A T	DET I	C T G
9 0	PHE ALA GLU PHE T T C G C C G A A T T T 510 510 500 510 ALA PRO HIS PHE LYS SER GLU LEU ALA PRO HIS PHE A A A T C A G A A T T A G C A C C G C A C T T 530 530	THR TRP THR SER ACTTGGACATCG 560 570 PRO ILE ARG LYS TYR SER ASP MET VAL ASN CCCATCGCAAATATTCAGATATGGTTAAT CCCATCGGAAATATTCAGATATGGTTAAT	VAL	G T G 620
ARG HIS CGTCAC 440 PR		ALA G C C	ALA	ວວອ
	LEU THR TTAACT	TYR	ГYS	A A A
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TYR CYS GLN ATTGCCAA 430	ARG TYR CGTTAT 490	GLU (3 A A G 550	LEU	T T A A 610
TYR CYS GLN MET TATTGCCAAATG 430	ARG C G C (LEU. I T A (ARG	່ນ
G G C 1	LEU TTA(GLY LEU GLU GLY TYR ALA THR TRP THR SER GGTTTAGAAGGCTATGCCACTTGGACATCG 550 560 570 PRO ILE ARG LYSCCCATCCGCAAAT	HIS	CATCGCTTAATCAAAGCCGTGCTGGCAAAA 610 620
-	=	=		

ASN ASP VAL	A A A T G A C G T G 660		ILE ALA ASP 5	. A T T G C C G A T C 720	ASN ALA GLU AATGCAGAA	
GIN	C A 650		ASP	G A 710	PHE TTTT 770	
PRO	CCA		ARG	L O J	GLU G A A	
LYS	A A A	•	ŒŨ	SAA	VAL 3. T. G.	
GIN PRO TYR GLU LYS	CAGCCTTATGAAAACCACAAAATGA. 640 650	LEU ALA ARG LEU GIN GLU SER ARG ARG GIN 6432.SL (TTGGCACGTTTGCAAGAGTCTCGCCGCCAA 670 680 690 ASN ARG LEU VAL GLU	A A T C G C C T A G T G G A A C G T G A T A T T G C C G A T N 710 720 720	TRP LEU TYR CYS ARG TYR LEU ALA ASP LYS TGGCTATATTGCCGTTATCTTGCTGACAAA 730 VAL ALA GLU ASN VAL GLU PHE ASN ALA GLUGTGGCTGAAATGTGGAATTTAATGCAGAA	VAL GIN ASP VAL MET ARG ALA GLY LEU ARG GTGCAAGATGTAATGCGTGCAGGCTTACGC 790 800 810

G.25D

FIG.25E	LEU GLU ASN GLY ALA SER I TCGAAAATGGTGCATCGC	LEU
PHE ILE PRO AL TTATTCCTGC 850	PHE ILE PRO ALA ALA THR LEU HIS ASN ASN TTTATTCTCTGCCGCCACGTTGCACAACA 850 860 870 LYS GLU GLU ILE GLN LEU ASN PRO ASP GLUAAAGAAGAAATACAGCTAAACCCTGACGAA	GLU GLU 900
LEU ALA LEU TY TCGCCTCTA 910	LEU ALA LEU TYR ILE LYS GLY GLU ARG THR CTCGCCCTCTATATAAAGGCGAACGCACT 910 930 TYR LYS ILE GLY ASP ILE VAL LYS VAL LYSTACAAAATAGGCGACATTGTGAAAGTGAAA	LYS A A A 960
LEU THR GLU VAL TCACAGAAGTG 970	LYS GLU ALA THR ARG SER A A A G A A G C A A C T C G C A G T 980 ILE VAL GLY GLU ILE LEU GIN *** LEU 1000 1000	PRO . C. C.

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d II	GAG 0	GLU	G A G
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) ASP GLY LYS THR AGACGCAAAAC 1040 1050	CGTTGTGAAAGTGGGCAATGAGTATTACGA	G G C G G A T A T G G A 1100 1100 LYS LYS VAL LYS LYS LYS LYS LYS LYS LYS L	T A A A A A G T C A A A A A T G G C G A G C T G G T G A A
THR A C 1050	0 T G	ASP 1.G A 1110 AL LYS	AAA
S TH A A C 1050	A A A (T AS 1110 VAL	
C A A	T G 7	T A T	A A (
GLY G G	. Đ ∐ .	ASF G A S 1	AA
ASP G A C 0	.C G T	ALA G C G 10	TAP.
PHE GIN TYR VAL THR GLÜ ASP GLY LYS THR TCCAATATGTTACGGAAGACGGCAAAC 1030 1040 1050	• • •	ALA LYS GLN ASP GLY SER ALA ASP MET ASP CCAAGCAAGACGGTTCGGCGGATATGGA (6295.SL 1100 1100 1110	:
THR ACG		ASP GLY G A C G G T C (6295.SL	
VAL GTT		ASP G A C	
TYR T A T 1030		GLN C A A 1090	
GLN C A A		LYS A A <u>G</u>	
PHE GIN TYR VAL THR GLÜ ASP GLY LYS THR GTTCCAATATGTTACGGAAGACGGCAAAAC 1030 1040 1050		ALA LYS GIN ASP GLY SER ALA ASP MET ASP A G C C A A G A C G G T T C G G C G G A T A T G G A C G T T C G G C G G A T A T G G A T A T G G A T A T G G A T A T	

GAAA VAL AACTAAAGTGAAATTGGTATCGGCAAACGG... TCCGGT ASIN ...TACAAA

GGAAGGCACGGAAGATACCGATGCGGTCAG....
1210 1230 VAL ALA ASP GEO GLY

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LYS A A 1260	GLY G G 1320	GLU GLU 1380
ASN A A C	VAL GTC	G G C
GLN C A A	ASP 3 A C	ASP G A C
LEU PTG(ALA 3 C C (THR ACA 0
ALA LI CCT' 1250	ASP AI 3 A T G C	SER TI
LYS , A A G	SER C C	LYS A A A T
PHE LYS GIN LEU LYS ALA LEU GIN ASN LYSCTTTAAGCAGTTGAAAGCCTTGCAAAACAA 1240 1250 1260	AGGTTACGTTAAGCGCGAGCAATGCTTA AGGTTACGTTAAGCGCGAGCAATGCTTA 1270 1280 1290 ALA ASN GLY GLY SER ASP ALA ASP VAL GLY 1310 1320	LYS VAL THR GIN THR LEU SER ASN GLY LEU AGGTAACTCAAACTTTAAGCAATGGTTT 1330 1340 1350 ASN PHE LYS PHE LYS SER THR ASP GLY GLU GAATTTAAATTTAAATCCACAGACGGCGA
	L T A L , ,	YL FAA
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	A A	LYS A

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TAAAGTGGGCAAACGTGCAGATGCAGGTAC...

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ASP G A C G
T G C G A C A A G A T 1460 LYS VAL AIA SER ASP GLY ILE SER ALA GLY T A A A G T G G C T T C A G A C G G C A T T A G C G G G G T A A A G T G A C G A C G C A T T A G C G C G G G T A A A G T G C T T C A G A C G G C A T T A G C G C G G G A A A G T G C T T C A G A C G G C A T T A G C G C G G G A A A G T G C T T C A G A C G G C A T T A G C G C G G G 1480
S ILE 1470 ALA S G C T T
A ASP LYS CGACAA LYS VAL AAAGTGG
ASP GAG SV
ASP ALA ASP LYS G A T G C C G A C A A G 1460 LYS VAL AI T A A A G T G C C
ASP G A T (146(
THR ACTG
ALA G C G
ALA G C G 1450
GLY ALA ALA ALA ' 3 G T G C G C G G A 1450
GLY ALA ALA THR ASP ALA ASP LYS ILE GGGGGGGGGGGGACTGATGCCGACAGGT 1450 LYS VAL ALA SIA 1480

FIG.25H

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ASN SN

TAATAAAGCAGTTAAAAACGTCGCGGCAGG	1510 1520 1530 GLU ILE SER ALA THR SER THR ASP ALA ILE ST C G A A A T T T C C G C C A C T T C C G A T G C G C G C G C G C G C G C G C G C G	ASN GLY SER GIN LEU TYR ALA VAL ALA LYS TARCGCAGTTGTATGCCGTGGCAAA 1570 1580 1590
TAATAA		ASN GLY <u>TA</u> ACGG

1800

CAAATTGATTAT

TTCCGATAATGG

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PRO 1 C C 1680	GLN C A	LEU
LEU TTA	GLY G G T	ARG
GIN	GLN C A A	in in its second and
SER ICA(TYR	ILE
ALA S 5 C T T 1670	SER A G T C	17.30 III OETI
ALA 3 C G C	SER AGT 1	LYS
ALA SER ALA LEU ALA ALA SER GIN LEU PROAGCAAGTGCATTAGCGGCTTCACAGTTACC 1660 1670 1680	TAAATCAATGGT 1700 1710 SER ILE ALA GLY SER SER TYR GLN GLY GLN TTCTATTGCGGGAAGTAATCAAGGTCA	I/20
ALA G C A 1 1660	T VA G G T 1710 ALA S C G C	1720 G II A A T 1770 ASN
SER AGTO	GIN ALA SER MET PRO GLY LYS SER MET VAL A C A A G C T C T A T G C G G T A A A T C A A T G G T 1690 1700 1710 SER ILE ALA GLY TT C T A T T G C G G G	SER GLY LEU ALA ILE GLY VAL SER ARG ILE A A G T G G T T T A G C T A T C G G G T A T C A A G A A T 1750 1760 1770 SER ASP ASN GLY
ALA 3 C A 1	S SE ATC SER	L SE
A	X LX 3 T A A 1700 T T	VA VA 1760
	19 0 0 0	15 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
	PRO C C G	ILE A T C
	MET A T G	ALA G C T
	SER T C T 1690	LEU T T A 1750
	ALA 3 C C	GLY 3 G.T
	GIN	SER
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...AGGCGTTGCAGCTGTTGGTTACCAGTG GTCAGGCACAATAGCCAAGGTAAAAC....
1810 1820 1830 ... GLY LYS GLY GIN SE ASIN GLY

GTAATAGAATTC 1870

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FIG.26A	
ATG AAC AAA ATT TTT AAC GTT ATT TGG AAT GTT GTG ACT CAA ACT TGG Met Asn Lys Ile Phe Asn Val Ile Trp Asn Val Val Thr Gln Thr Trp 2130	48
GIT GIC GTA TCT GAA CTC ACT CGC ACC CAC ACC AAA TGC GCC TCC GCC Val Val Val Ser Glu Leu Thr Arg Thr His Thr Lys Cys Ala Ser Ala 2145	96
ACC GTG GCG GTT GCC GTA TTG GCA ACC CTG TTG TCC GCA ACG GTT GAG Thr Val Ala Val Ala Val Leu Ala Thr Leu Leu Ser Ala Thr Val Glu 2160	144
GCG AAC AAC AAT ACT CCT GTT ACG AAT AAG TTG AAG GCT TAT GGC GAT Ala Asn Asn Asn Thr Pro Val Thr Asn Lys Leu Lys Ala Tyr Gly Asp 2180	192
GCG AAT TIT AAT TIC ACT AAT AAT TCG ATA GCA GAT GCA GAA AAA CAA Ala Asn Phe Asn Phe Thr Asn Asn Ser Ile Ala Asp Ala Glu Lys Gln 2195	240
GTT CAA GAG GCT TAT AAA GGT TTA TTA AAT CTA AAT GAA AAA AAT GCG Val Gln Glu Ala Tyr Lys Gly Leu Leu Asn Leu Asn Glu Lys Asn Ala 2210	. 588

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336	384	432	480	528	576
AGT GAT AAA CTG TTG GTG GAG GAC AAT ACT GCG GCG ACC GTA GCC AAT	TTG CGT AAA TTG GGC TGG GTA TTG TCT AGC AAA AAC GGC ACA AGG AAC	GAG AAA AGC CAA CAA GTC AAA CAT GGG GAT GAA GTG TTG TTT GAA GGC	AAA GGC GGT GTG CAG GTT ACT TCC ACC TCT GAA AAC GGC AAA CAC ACC	ATT ACC TTT GCT TTA GCG AAA GAC CTT GGT GTG AAA ACT GCG ACT GTG	AGT GAT ACC TTA ACG ATT GGC GGT GGT GCT GCT GCA GGT GCT ACA ACA
Ser Asp Lys Leu Leu Val Glu Asp Asn Thr Ala Ala Thr Val Gly Asn	Leu Arg Ly's Leu Gly Trp Val Leu Ser Ser Ly's Asn Gly Thr Arg Asn	Glu Lys Ser Gln Gln Val Lys His Ala Asp Glu Val Leu Phe Glu Gly	Lys Gly Gly Val Gln Val Thr Ser Thr Ser Glu Asn Gly Lys His Thr	Ile Thr Phe Ala Leu Ala Lys Asp Leu Gly Val Lys Thr Ala Thr Val	Ser Asp Thr Leu Thr 11e Gly Gly Gly Ala Ala Ala Gly Ala Thr Thr
2225	2240	2260	2285	2290	2305

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624	672	720	768	816	864
ACA CCG AAA GTG AAT GTA ACT AGT ACA ACT GAT GGC TTG AAG TTC GCT	AAA GAT GCT GCG GGT GCT AAT GGC GAT ACT ACG GTT CAC TTG AAT GGT	ATT GGT TCA ACC TTG ACA GAC ACG CTT GTG GGT TCT CCT GCT ACT CAT	ATT GAC GGA GGA GAT CAA AGT AGG CAT TAC ACT CGT GCA GCA AGT ATC	AAG GAT GTC TTG AAT GCG GGT TGG AAT ATC AAG GGT GTT AAA GCT GCC	TCA ACA ACT GGT CAA TCA GAA AAT GIC GAT TIT GIT CAT ACT TAC GAT
Thr Pro Lys Val Asn Val Thr Ser Thr Thr Asp Gly Leu Lys Phe Ala	Lys Asp Ala Ala Gly Ala Asn Gly Asp Thr Thr Val His Leu Asn Gly	Ile Gly Ser Thr Leu Thr Asp Thr Leu Val Gly Ser Pro Ala Thr His	Ile Asp Gly Gly Asp Gln Ser Thr His Tyr Thr Arg Ala Ala Ser Ile	Lys Asp Val Leu Asn Ala Gly Trp Asn Ile Lys Gly Val Lys Ala Gly	Ser Thr Thr Gly Gln Ser Glu Asn Val Asp Phe Val His Thr Tyr Asp
2320	2340 2345	2355	2370	2385	2400

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912	096	1008	1056	1104	1152
ACT GIT GAG TIC TIG AGT GCG GAT ACA GAG ACC ACG ACT GIT ACT GITA. Thr Val Glu Phe Leu Ser Ala Asp Thr Glu Thr Thr Thr Val Thr Val 2420	GAT AGC AAA GAA AAC GGT AAG AGA ACC GAA GTT AAA ATC G3T GCG AAG	ACT TCT GIT ATC AAA GAA AAA GAC GGT AAG TITA TITI ACT GGA AAA GCT	AAC AAA GAG ACA AAT AAA GITT GAT GGT GCT AAC GCG ACT GAA GAT GCA	GAC GAA GGC AAA GGC TTA GTG ACT GGG AAA GAT GTG ATT GAC GCA GTG	AAT AAG ACT GGT TGG AGA ATT AAA ACA ACC GAT GCT AAT GGT CAA AAT
	ASD Ser Lys Glu Asn Gly Lys Arg Thr Glu Val Lys 11e Gly Ala Lys	Thr Ser Val 11e Lys Glu Lys Asp Gly Lys Leu Phe Thr Gly Lys Ala	Asn Lys Glu Thr Asn Lys Val Asp Gly Ala Asn Ala Thr Glu Asp Ala	ASP Glu Gly Lys Gly Leu Val Thr Ala Lys Asp Val Ile Asp Ala Val	Asn Lys Thr Gly Trp Arg Ile Lys Thr Thr Asp Ala Asn Gly Gln Asn
	2435	2450	2465	2480	2500 2500

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1200	1248	1296	1344	1392	1440
GGC GAC TTC GCA ACT GTT GCA TCA GGC ACA AAT GTA ACC TTT GCT AGT	GGT AAT GGT ACA ACT GCG ACT GTA ACT AAT GGC ACC GAT GGT ATT ACC	GIT AAG TAT GAT GCG AAA GIT GGC GAC GGC TTA AAA CTA GAT GGC GAT	AAA ATC GCT GCA GAT ACG ACC GCA CTT ACT GTG AAT GAT GGT AAG AAC	OCT AAT AAT CCG AAA GGF AAA GTG OCT CAT GTF OCT TCA ACT GAC CAG	AAG AAA TIG GIT ACA GCA AAA GGF TIA GIA ACA GCC TIA AAC AGF CIA
Gly Asp Phe Ala Thr Val Ala Ser Gly Thr Asn Val Thr Phe Ala Ser	Gly Asn Gly Thr Thr Ala Thr Val Thr Asn Gly Thr Asp Gly 11e Thr	Val Lys Tyr Asp Ala Lys Val Gly Asp Gly Leu Lys Leu Asp Gly Asp	Lys Ile Ala Ala Asp Thr Thr Ala Leu Thr Val Asn Asp Gly Lys Asn	Ala Asn Asn Pro Lys Gly Lys Val Ala Asp Val Ala Ser Thr Asp Glu	Lys Lys Leu Val Thr Ala Lys Gly Leu Val Thr Ala Leu Asn Ser Leu
2515	2530	2545	2560 2575	2580	2600

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1488	1536	1584	1632	1680	1728
AGC TOG ACT ACA ACT OCT GAG GGG GAC OGT OGT AGG CTT GAT GGA Ser Trp Thr Thr Ala Ala Glu Ala Asp Gly Gly Thr Leu Asp Gly 2610	AAT GCA AGT GAG CAA GAA GTT AAA GCG GGC GAT AAA GTA ACC TITT AAA Asn Ala Ser Glu Gln Glu Val Lys Ala Gly Asp Lys Val Thr Phe Lys 2625	GCA GGC AAG AAC TITA AAA GIG AAA CAA GAG GGF GGG AAC TITF ACF TAF Ala Gly Lys Asn Leu Lys Val Lys Gln Glu Gly Ala Asn Phe Thr Tyr. 2640	TCA CTG CAA GAT GCT TTA ACA GGC TTA ACG AGC ATT ACT TTA GGT ACA Ser Leu Gln Asp Ala Leu Thr Gly Leu Thr Ser Ile Thr Leu Gly Thr 2660 2670	GGA AAT AAT GGT GCG AAA ACT GAA ATC AAC AAA GAC GGC TTA ACC ATC Gly Asn Asn Gly Ala Lys Thr Glu Ile Asn Lys Asp Gly Leu Thr Ile 2675	ACA CCA GCA AAT GGF GCG GGF GCA AAT AAT GCA AAC ACC ATC AGC GTA Thr Pro Ala Asn Gly Ala Asn Asn Asn Asn Thr Ile Ser Val 2690
A W	A A	OAV	E W	Ø 0	计为

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FIG.26G	
ACC AAA GAC GGC ATT AGT GCG GGC GGT CAG TCG GTT AAA AAC GTT GTG Thr Lys Asp Gly Ile Ser Ala Gly Gly Gln Ser Val Lys Asn Val Val 2705	1776
AGC GGA CTG AAG AAA TITT GGT GAT GCG AAT TTC GAT CCG CTG ACT AGC Ser Gly Leu Lys Lys Phe Gly Asp Ala Asn Phe Asp Pro Leu Thr Ser 2720 2730	1824
TCC GCC GAC AAC TTA ACG AAA CAA AAT GAC GAT GCC TAT AAA GGC TTG Ser Ala Asp Asn Leu Thr Lys Gln Asn Asp Asp Ala Tyr Lys Gly Leu 2740	1872
ACC AAT TIG GAT GAA AAA GGT ACA GAC AAG CAA ACT CCA GTT GTT GCC Thr Asn Leu Asp Glu Lys Gly Thr Asp Lys Gln Thr Pro Val Val Ala 2755	1920
GAC AAT ACC GCC GCA ACC GTG GGC GAT TTG CGC GGC TTG GGC TGG GTC ASP ASN Thr Ala Ala Thr Val Gly Asp Leu Arg Gly Leu Gly Trp Val 2770	1968
ATT TCT GCG GAC AAA ACC ACA GGC GCC TCA AGG GAA TAT CAC GAT CAA Ile Ser Ala Asp Lys Thr Thr Gly Gly Ser Thr Glu Tyr His Asp Gln 2785	2016

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2304	AAT ACA GIT GCT GCG AAA TAT CAA GAT AAA GGT GGC AAA GIC GIT TCT Asn Thr Val Ala Ala Lys Tyr Gln Asp Lys Gly Gly Lys Val Val Ser 2880 2895
2256	AAA GAG GAT ATT GAC TTA ACA ACA GGT CAG CCT AAA TTA AAA GAT GGC Lys Glu Asp Ile Asp Leu Thr Thr Gly Gln Pro Lys Leu Lys Asp Gly 2865
2208	AAT GGA AAG GAA ACG AGC CTG GTT AAA GTT GGC GAT AAA TAT TAC AGC Asn Gly Lys Glu Thr Ser Leu Val Lys Val Gly Asp Lys Tyr Tyr Ser 2850
216(OCT AAA GGF GAA GTG GTT AAA TCG AAT GAA TTT ACC GTC AAA GAA ACC Ala Lys Gly Glu Val Lys Ser Asn Glu Phe Thr Val Lys Glu Thr 2835
2113	GTT TCC GGT AAA ACG GTC AAC GGT AGG CGT GAA ATT ACT TTT GAA TTG Val Ser Gly Lys Thr Val Asn Gly Arg Arg Glu Ile Thr Phe Glu Leu 2820
206	GIT CGG AAT GCG AAC GAA GTG AAA TTC AAA AGC GGC AAC GGT ATC AAT Val Arg Asn Ala Asn Glu Val Lys Phe Lys Ser Gly Asn Gly Ile Asn 2800 2805

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2352	2400	2448	2496	2544	2592
GIA AUG GAI AAT ACT GAA GCT ACC ATA ACC AAC AAA GGT TCT GGC TAT	GTA ACA GGT AAC CAA GTG GCA GAT GCG ATT GCG AAA TCA GGC TTT GAG	CTT GGC TTG GCT GAT GAA GCT GAT GGG AAA CGG GGG TTT GAT GAT AAG	ACA AAA GCC TIA TCT GCT GGT ACA ACG GAA ATT GIA AAT GCC CAC GAT	AAA GTC CGT TTT GCT AAT GGT TTA AAT ACC AAA GTG AGC GCG GCA AGG	GTG GAA AGC ACC GAT GCA AAC GGC GAT AAA GTG ACC ACA ACC TTT GTG
Val Thr Asp Asn Thr Glu Ala Thr Ile Thr Asn Lys Gly Ser Gly Tyr	Val Thr Gly Asn Gln Val Ala Asp Ala Ile Ala Lys Ser Gly Phe Glu	Leu Gly Leu Ala Asp Glu Ala Asp Ala Lys Arg Ala Phe Asp Asp Lys	Thr Lys Ala Leu Ser Ala Gly Thr Thr Glu Ile Val Asn Ala His Asp	Lys Val Arg Phe Ala Asn Gly Leu Asn Thr Lys Val Ser Ala Ala Thr	Val Glu Ser Thr Asp Ala Asn Gly Asp Lys Val Thr Thr Thr Phe Val
2900 2910	2920	2930	2945	2960 2975	2985

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2640	2688	2736	2784	2832	2880
AAA ACC GAT GTG GAA TTG CCT TTA ACG CAA ATC TAC AAT ACC GAT GCA	AAC GGT AAG AAA ATC ACT AAA GTT GTC AAA GAT GGG CAA ACT AAA TGG	TAT GAA CTG AAT GCT GAC GGT ACG GCT GAT ATG ACC AAA GAA GTT ACC	CTC GGT AAC GTG GAT TCA GAC GGC AAG AAA GTT GTG AAA GAC AAC GAT	GGC AAG TGG TAT CAC GCC AAA GCT GAC GGT ACT GCG GAT AAA ACC AAA	GGC GAA GTG AGC AAT GAT AAA GTT TCT ACC GAT GAA AAA CAC GTT GTC
Lys Thr Asp Val Glu Leu Pro Leu Thr Gln 11e Tyr Asn Thr Asp Ala	Asn Gly Lys Lys Ile Thr Lys Val Val Lys Asp Gly Gln Thr Lys Trp	Tyr Glu Leu Asn Ala Asp Gly Thr Ala Asp Met Thr Lys Glu Val Thr	Leu Gly Asn Val Asp Ser Asp Gly Lys Lys Val Val Lys Asp Asn Asp	Gly Lys Trp Tyr His Ala Lys Ala Asp Gly Thr Ala Asp Lys Thr Lys	Gly Glu Val Ser Asn Asp Lys Val Ser Thr Asp Glu Lys His Val Val
2995	3010	3025	3040	3060	3075

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2928	2976	3024	3072	3120	3168
AGC CIT GAT CCA AAT GAT CAA TCA AAA GGT AAA GGT GTC GTG AITT GAC	AAT GIG GCT AAT GGC GAT ATT TCT GCC ACT TCC ACC GAT GCG ATT AAC	GGA AGT CAG TIG TAT GCT GIG GCA AAA GGG GIYA ACA AAC CTT GCT GGA	CAA GTG AAT AAT CTT GAG GGC AAA GTG AAT AAA GTG GGC AAA CGT GCA	GAT GCA GGT ACA GCA AGT GCA TTA GCG GCT TCA CAG TTA CCA CAA GCC	ACT ATG CCA GGT AAA TCA ATG GTT GCT ATT GCG GGA AGT AGT TAT CAA
Ser Leu Asp Pro Asn Asp Gln Ser Lys Gly Lys Gly Val Val 11e Asp	Asn Val Ala Asn Gly Asp Ile Ser Ala Thr Ser Thr Asp Ala Ile Asn	Gly Ser Gln Leu Tyr Ala Val Ala Lys Gly Val Thr Asn Leu Ala Gly	Gln Val Asn Asn Leu Glu Gly Lys Val Asn Lys Val Gly Lys Arg Ala	Asp Ala Gly Thr Ala Ser Ala Leu Ala Ala Ser Gln Leu Pro Gln Ala	Thr Met Pro Gly Lys Ser Met Val Ala Ile Ala Gly Ser Ser Tyr Gln
3090	3105	3120	3140	3155	3170 3177

ALC CANDOILS

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FIG.26L
GGT CAA AAT GGT TTA GCT ATC GGG GTA TCA AGA ATT TCC GAT AAT GGC Gly Gln Asn Gly Leu Ala 11e Gly Val Ser Arg 11e Ser Asp Asn Gly 3185
AAA GTG ATT ATT COC TTG TCA GOC ACA ACC AAF AGF CAA GGF AAA ACA Lys Val 11e 11e Arg Leu Ser Gly Thr Thr Asn Ser Gln Gly Lys Thr 3200
GGC GITT GCA GGT GITT GGT TAC CAG TGG Gly Val Ala Ala Gly Val Gly Tyr Gln Trp 3220

FIG.27A

TC LCCMA OM

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AMOPEMPETAQOIHWI HOFTKARIQMRKIHSI FFKEKPDYAFVI AENGKVOEIKAEYRRIANOIVEEAMI IA PIPAAIPETAQQIHMLHQFTKARIQMRKIHSLFFKEKPDYAFVLAENGKVQEIKAEXRRIANQIVEEAMII ORF with HI1733 from H. influenzae strain Rd NICAAQFIHEQAKIGIFNAHSGFIKKYLENAHHFIMANLANEQNQTELAERYSVENLATINGYCOMRHDIEI NICAAQFI HEQAKTGI FNIHSGFTKKFI ENAHNFI MANLANEQNQI EI AERYSVENLATI NGYOQMRHDI EF IESDYLEI RLRRYLTFAEFKSEI APHFGLGI JESYATWISPIRKYSIJMANHRLIKAVI AKQPYEKPQAIALAR LESDYLELRRYLIFAEFKSELAPHFGLGLEGYAIWISPIRKYSIMMFRLIKAVLAKQPYEKPQNIMLAR LOEARRONKLNERDIAIMLYCRYLADKVASNAEFEAEVODANRAGIRVOILENGASLFIPAATIHNNKEEIQ LOESRRONRLVERDIADMLYCRYLADKVAENVEFNAEVODVMRACI RVOLLENGASLFIPAATI HNNKEETI 360 2, Alignment of NIHi strain 12

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named as homolog to a protein from Escherichia coli ##cross-references GB:L42023; TIGR:HI1733 LNPDELALY INGERIYKIGDIVKVNLITEVKEAITRSIVGEILQ LNPDELALYIKGERIYKIGIMVKVKLITEVKEAIRSIVGEILQ ##note

#checksum 8365 MFQUNPLLAQLKQQIHDSKEQVEGVVKSIDKAYGFLECDKKIYFTAPPSMKKVMKAXLKATIEKQGDKE QAEPEAL I EPVILIRF I AKVRFNKDKKI QVI VIZHPSINQP I GAQQAKSVKEET QEGDWVANILKI HPIRDD RFFYATINQLICRADDELAEWWILARHEQSRYFVRGAEPYEMLDQKIRENLIFALHEVTIDSESIMIMDD ALYTEPTAQNSTQTGWKLVVALADPTAYTALDSQTEQEAKQRCFTNYLFGFNIFMLPRELSDFLCSLIAN HSGFDKKFLENAHNFLMANLANEQNQTELAERYSVENLATINGYCQMRHDIEPIESDYLELRLRRYL1FA ALMLYCRYLADKVASNAEFEAEVQDVMRAGI RVQLLENGASLFTPAATLHNNKEETQLNPDELALYTKGE ETRPALVCYTETDLIGNITTAKPHFVSAYVQSKAKLAYNKVSDYLEQALNAWQPEMPETAQQIHMLHQFTK ARI QMRKTHSLFFKEKPDYAFVLAENJKVQETKAEYRRIANQIVEEAMI IANICAAQFI HEQAKTGIFNI EFKSELAPHFGLGLEGYATWISPIRKYSIYMMHRLIKAVLAKQPYEKPQMIVLARLQEARRQMRLVERDI #molecular-weight 75782 #length 659 RIYKIGIMVKVKLIEVKEAIRSIVGEILQ SUMMARY A64139

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RTAPVLSFHSDKEGTGEKEVTENSWAGTYFTNKGVLKA-

FIG.28A

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RTAPVILSTHSDKBJTGEKEVTENSIMGIYFHNKGVILKY GSAYAQKKOJTKHIAJGEQNOPRESGTAKADGJTAJTLK GSAYAQKKOJTKHIAJGEQNOPRESGTAKADGJTAJTLK GSAYAQN-NSK-AIFGTTQNDNASASUEASIAJG KIKQSTNASSFTYSLKKOLITDLTSVATEKLSFCANGDKVDITSDANG KIKQSTNASSFTYSLKKOLITDLTSVATEKLSFCANGDKVDITSDANG KKKQSTNASSFTYSLKKOLITDLTSVATEKLSFCANGDKVDITSDANG WG-SSLIKIGTDITQGESIAJGGDVKASGDASIAJGSDDLHLLDQHGNPK. PRNQAANQKAGSHAKGKESIAJGGDVLABGDASIAJGSDDLYLDFNSTNGK. * * * * * * * * * * * * * * * * * * *	A		33 32 29 K22 M4071
	GIFVKVQSTEDDIEDSAATKDINKOQALKAGDILJILKAGSAYAQKKDIKHIAIGEQNQPRRSGTAKADGDRALAIGENANAQOGGSAYAQN-NSK-AIFCTTGNNINASAGNEASIAIGSIAKAHAN	VASSFTYSLKKDLTDLTSVATEKLSFGANGDKVDITSDANG. VASSFTYSLKKDLTDLTSVATEKLSFGANGDKVDITSDANG. VASSFTYSLKKDLTDLTSVATEKLSFGANGDKVDITSDANG. VASSFTYSLKKDLTDLTSVATEKLSFGANGDKVDITSDANG. STIDTTQGESTATGGDVKASGDASIAIGSDDLYLDRNSTNSK. SSHAKGKESTATGGDVLAEGDASIAIGSDDLYLDRNSTNSK.	

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The second secon	2
IALAKIGNANVHINGIDSTIPDAVINIGVISSSS-FTPADVEKTR	HSF
LKLAKTOANA-VHINGLOSTLPDAVINIGVLSSSS-FTPNIVERTR LKLAKGINGDTAVHING ASTRIPTATTANTS GTGVT-FCDCDIEGTED	API
HPKGTLINDLINGHAVLKEIRSSKDNDVKYRRTTASGHASTAVGAMS	rd 4223
YFNGLLSTLIQN-HTVLRQIRDGNGSQ-KYRRTAABGHASTANGAMA	LES-1
* ** **	
ATVKDVI NAGANI KGAKTAGANVESVDI VSA YNNVEFI TGDKNIT DVVI TAKENGKITEVK	
ATIKDVINAGANIKGAKVAGANTESVDIVAGATANNVEFITGDKNILLVVVIITAKNITIRKKTITEVK	
AQCHESIVAFOTRA-TAKSAYSLAVGLAATAEOQSTTALGSDATSSSLGALALGAGTRAOLO	
AKGHFANAFCTRS-TABENYSKAVGLTAKAEKGYTIAIGSNAQAINYGALALGADTRVDLD	
** * * *** * * * * * *	
	33
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	M4071 11
FTPKTSVIKEKDGKLFTGKENNDTNKVTSNTAFTPKTSVIKEKDGKLFTGKENNDTNKVTSNTAFTPKTSVIKINNGKLLFTGKQIKDANIGTATNAGSIALGQGSVVTQSD-NNSRPAYTPNTQALDPKFQ-ATNANIKAGPLSIGYGIALGYGSQIIANNANNKAYVPBGAGSNIKSSKATGAGIFSIG	K9 HSF API Rd 4223 LES-1
TINIDEGNGLVTAKAVI - DAVNKAGMIVKTTTANGQNGDFATVASGINVIFESGDGTTASVT TINIDEGNGLVTAKAVI - DAVNKAGMIVKTTTANGQNGDFATVASGINVIFESGDGTTASVT TEDTDEAMA*	
*RYRRANGLVTAKTVI-EANNKSGMRVKTTTANGQNDDFATVASGINVTFANANGTTASVT SNSIKRKI INVGAGVNKTDAVNVAQLEAVVKMAKERRITFQGDDNSTDVKIGLDNTLTIKGG SSTIKRKI INVGAGYEDTDAVNVAQLKAVENLAK-RQITFKGDDNSTGVKKUGETLTIKGG * *** * *** *	
	33

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GKVAETAKEDDKKKLVNAGDLVTALGNLSMKAKAEADTD--CALEGISKDQEVKAGETVTFK... GKVAETAKEDDKKKLVNAGDLVTALGNLSMKAKAEADTDTDGALEGISKDQEVKAGETVTFK... GKVAETAKEDDKKKLVNAGDLVTALGNLSMKAKAEADTD--CALEGISKDQEVKAGETVTFK... NATTTVKVGSSSSTTAETLSDSLTFTQPNTGSQSTSKTVYGNAGVKFTNNAETTAALGTT-R...

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32 29 K22 M4071 111 K9 HSF API API Rd 4223 LES-1

FIG.28E

KTVINKDGLFITPAGNGGTTGTNTISBTKDGIK..NKAI..VASGLRAYDDA..DVL...AT..

--. ASV.CR..... D-T. TK.. A.... --N--.PV..K.KA..D-A.F..--T..... --T.G..S..G.KA..ST..P...A.G..AT.

--N--.SV..G..A..D---T...TT.

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AGSTITCHNSLNVYGK-NNSNFNSANNSIA..

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... AGKNILKVKQDGANFTYSIQDALTGLTSATLGGTTINGGNDA ...ITKDKIGFSNKAGTVDENKPYLDKDKLKVGNSTINNGGLT .. AGRNILKVKODGANFTYSLODALTGL/TSATLOGTTNOGANDA ... ACKNILKVKQDGANFTYSLQDALITGLITSATILGGITINGGNDA TASEKVIVGSGAN-TAELQSGGLIFT-PITNA-STDKTVYGTDGLKFTDNSN-TALEDITI-R... ...ITRDKIGFARD-GDVDE------

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		33	32	29	K22	M407	11	2	HSF	API	B	4223	LES-1						
VNIVIIGGSNKQIQVGADGIKFADVNVNVSNAAKFGITRITEEEIGFAD	60.00000000000000000000000000000000000	DIAKONDSVYDGILANIANEKGTDKSKFLVADETTATVGANLRKL	ATDENED. EELEPVORSV	E.HVQDA.KD.NSN.A	E.HVQDA.KD.N.SN.A	AR.F.GADAN.N-L.T.DKA	AEVQEA.KNAS-D.LE.N.AD		RHVEDA.KNAN.QPT.S.AD	RHVEDA.KNAN.QPTDS.AD	RHVEDA.KNAN.QPS.AD	KQAP.IDKKQ.KVGSVAITIDNGI.AGNKKISA.GSSANDA	GKVDKK.P.LDKKQ.QVG.VKIT.DSGINAGDQKISNVKDATDDTDA	* * * * *	130 140 150 160	GWVSTRNSTKEE-SNQVKQADEVLFEG-KDGVTVTSKSENCKHTVT	N.SFNSANBULG. QEALLEVELLEN TSGAA S. S. KD T	L.SG.RN.K.YTSGAAS.S.KDI	

FIG.28G

KTVINKDGLTITPAGNOGTIGINFISBTKDGIK..NKAI..VASGLRAYDDA..DVL...AT... KTVINKDGLTITPAGNOGTIGINFISBTKDGIK..NKAI..VASGLRAYDDA..DVL...AT...

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.....I.VSVAETKADCGLEKD

.....T. -AGAA.....

...K.S.G..Q...T.....AI.-----

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. GDTIKLKVDNQNIDNVLIVGNNSTAVIKGGFEIVKTGATDADRGKVT . GDTIKLKVINQNIDAVLITVGANGTAVIKGGFEIVKIGATDADRGKVT ..SCINNSLVTAEHLASYINEVNRTADSALQSF-TVKEED-DDDANAIT ..GDTIKLKVDNQNTDNVLIVGNNGTAVIKGGFEIVKTGATDADRGKVT /TIEQL.AAKPIINAGAGISVIPPTEISVDAKSGN..APTY.IGVKT.EINSDGTSDKFSVKG.G....-T.-AGAA.....I.VSVAETKADSGLEXDG....-T.-AGAA.....I.VSVAETKADSGLEXD.

FIG.28H

..L.S..G.RN.K.Q...H.. ..L.S..G.RN.K.Q...H..GKEN.K.Q...H..

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FIG.281		
VKDATANDADKKVATVKDVATAINI VKDATANDADKKVATVKDVATAINI	VKDATANDADKKVATVKDVATAINSAATEVKTENLITISIDEINPIDNGKODALKAGDILITEK VKDATANDADKKVATVKDVATAINSAATEVKTENLITISIDEINPIDNGKODALKAGDILITEK	•
VAKDITKNAGAVSILKIKGKNGLIN LYSKANTPNIFETITFA-GENGIS:	VALATIANDELIKVATVADVATALINSAATEVKIENLITALDEALAKUUS-DDALKASDILITEK VAKDITKNAGAVSILKIKGKNGLIVATKKO-GIVITGILSQDSGLITIGKSIINNDGLIVKDIN LYSNGNIPNIFETITFA-GENGISISNDIAKGKVKVGIDPINGLITPKLIVGSDKDGKTQLV	
**	* * * * *	33
	35	2333
	M	M407
	AGKNI.KVKRDGKNITFDI.AKNI.EVKTAKVSDTI.TIQANTPTGGTTAT HEAGKNI.KVKRDGKNITFDI.AKNI.EVKTAKVSDTI.TIQANTPTGGTTAT AI	PPI HSPI
	LEVKTATFSDRLTIG	Rd 4223
	IBQVASGATIR	LES-

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FIG.28J	
PKVNITSTADGINFAKETADASGSKNVYLKGIATTLITEPSAGAKSSHVDINVDATK-KSNAA PKVNITSTADGLNFAKETADASGSKNVYLKGIATTLITEPSAGAKSSHVDINVDATK-KSNAA	
PYLDQDKLQVGNVKITINIGINAG3KAITGLSPTLPSIADQSS-RNIELGNTI-QDKDKSNAA ********************************	
	33
	32 23 23 24 25
	M4071
SIEDVLRAGWINQCANANNUDYVATYDIVNFTDDSTGTTTVTVTVTQKADG	KS API
SIGDIINIGENIKANSNSYGEVSTYNIVDFIDAVATTAKVIY-DEINO	4223 LES-1

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FIG.28K		
*** **** * *** * * * * * * * * * * * * *	* * *	
KGADVKIGAKTSVIKDHNGKLFTGKDLKDANNGATVSEDDGKDTGTGLVTAKTVIDAVNKSG KGADVKIGAKTSVIKDHNGKLFTGKDLKDANNGATVSEDDGKDTGTGLVTAKTVIDAVNKSG		
TSKVYVDVNVDEKTIELIGDNGKINKLGVKTTTLIKTIDANGNIPTNFHVNSSDEDALVNAKDI TSKVTYDVNVDEKTIELIGDNGKINKLGVKTTTLITINANGK-ATNF-STITANDALVNAKDI *		
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		32 29
		Z \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \
	1 1 1	‡ <u>2</u>
MRVTGEGATAETGATAVNAGABETVTSGTSVNFKNEARTTATVSKDNGNIN	TVSKDNGNIN	E A
;		至

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	4223 LES-1	:				33	29 K22	M4071	
FIG.28L	IAENINITAKETHTIKGTADTALQIFTVKKVDENNNADDANALTAENINTLAKETHTITKGTADTALQIFKVKKDGATDDETLT			VKYDVNVGDGI.KIGDDKKIVADTITILIVIGGKVSVPAGANSVNNNRKT.VNAEGI.ATAINNIS VKYDVNVGDGI.KIGDDKKIVADTITILIVIGGKVSVPAGANSVNNNRKT.VNAEGI.ATAINNI.S	VGKDSTQNGKTVNITALKGENGLIVATNKDSTVTFGIN				

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WTAKADKYADGESEGETDQEVKAGDKVTF-KAGKNLKVKQSEKDFTYSLQD	API
TTSGLKAGKST-INDGGLSIKNPTGSEQIQVGADG	Kd 4223 LES-1
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TLIGLISITLGGTANGRNDIGIVINKDGLITITLANGAAAGIDASNGNIISVIKDGISA TLIGLISITLGGTANGRNDIGIVINKDGLITITLANGAAAGIDASNANIISVIKDGISA	
VKFAKVNNNSVVGAGIDGTIRITRDEIGFTGINGSLDKSKPHLSLDGINA VKFAKVDK-GNSSTGIDGTSRITRDQIGFTGANGSLDTIRPHLIRDKLKVGEVEITNTGINA * * * * * * * * * * * * * * * * * *	
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K9 HSF API Rd 4223 LES-1

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		: : :	: : : :	: :	
LKTYKOTQNTA LKTYKOTQNTA	HDAVTGGKIYDLKT NDAVTGGRVYDLKT *** * * *			RGLGWILSAKKTADE.	
GNKEITNVKSA	GGKKITINIQSGEIAQNSHDAVTGGKIYDLKT GGKKITINIQSGDITQNSNDAVTGGRVYDLKT * * * * * * * * * * * * * * * * * *			JDLTK PATCAACAVCADAKAPDTTAATVGDLRGLGAVLSAKKTADE	
				DLTKPATGAA	: : :

FIG.28N

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GATQPAANTAEVAKQDL

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--ISVIKGSFAEVKT

DANGKHTVTI DVAEAKVGDGLEKDIDGK I KLIVDNIDGANI LIVDATKGASVAKGEFNAVTT DANGKHTVTI DVAEAKVGDGLEKDIDGK I KLIVDNIDGANI LIVDATKGASVAKGEFNAVTT

SNPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVGNUNGKGIVIDS SNPYSSYDTSKTSDVITFAGENGITTKVNKGVVRVGIDQTKGLTTPKLTVGNUNGKGIVIDS

M4071 11 K9 HSF SPI: Rd 4223 1ES-1

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... DATTGGQVNIAD-RGKVK----AEDENGADVDKKV

FIG.280

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K22 M4071 11 K9 K9 HSF API Rd

DATTICGQVNAD-RCKVK----AEDENGADVDKKV----DATTIAQCTNANERCKVVVKGSNCATATETDKRKV---DATTIAQCTNANERCKVVVKGSNCATATETDKRKV---ONGQNTTTGLSNTLANVTNDKGSVRTTEQCALI IKDEDKTRA
KDCQNTTTGLSNTLANVTNDCAGAISLS-QGLAN-DTDKTRA

ININIDSSGNAVGSSTITFKAGDNIKIKOSGN.
ATVKDVAKAINDAAIFVKVESTDDDIENCAAGKNETTDQALKAGDTIJIKAGKNIKAKLDQN.
ATVKDVAKAINDAAIFVKVESTDDDIENCAAGKNETTDQALKAGDTIJIKAGKNIKAKLDQN.

ATVGDVAKAINDAATFVKVEN-DDSATIDDSPTDDCANDALKAGDTL/TLKAGKNLKVKRDG-...
ATVGDVAKAINDAATFVKVEN-DDSATIDDSPTDDCANDALKAGDTL/TLKAGKNLKVRRDG-...

ASIVDVLSAGENLQGNGEAVDFVSTYDTVNFADGARTTAKVTYDDTSKTSKVVYDVAVDDTT. ASIGDVLARGENLQGNGEAVDFVSTYDTVDFIDGARATTAKVTYDDTSKTSKVVYDVAVDVKT.

FIG.28P

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210 220 240 250

LKFAKÇGT-NGONGN-VHINGIASTILDDPRVGGKTAHLTKEISDTERN--RAASVGDVIANA.

L. T.NG. S.-- T.TILA.T.G.VDTN.DAVNYH--- Q. S.

L. T.NG. -- T.TIT.MT.QASNGVAVQ-NH--- A.

L. T.NG. -- T.TIT.MT.QASNGVAVQ-NH--- A.

PS.-- T.TIT.TTKSATNGVDVQNH--- A.

PS.-- T.TIT.TTKSATNGVDVQNH--- A.

V. GA.GANGDIT-- TN. Q.TILNTGAVSKILDGRGSTTANEKK. Q. S.

DSKT-DDA.--I. T.TILNSGATTNIGGRGSTTDNEKK. K.

KKTTVRVDVTGL

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300	VITIDDIN	A.TAH-	TAH-	TAH-	TAHN	IV.V.S	V.S	VES	VES	• • • • • • • • • • • • • • • • • • • •	WN.A	WN.A					
290 300	GMIRGAKTIGG-TVDNVDFVSTYDIVEFASGANANVSVTTDDN	Q.NAMVDFVR.Y.TNA.TAH-	Q.NGASVDFVNAY.TNT.T.T.NTAH-	Q.NGASVDFVMAY.TNT.T.TNTAH-	Q.NGASTAHN	K.V.AGSTT-GQSEHLDIETTTV.V.S	K.V.TGATSRLSEETTLV.S	VV.PASANNQE.IAD.VDKDTTVES	VV.PASANNQE.IAD.VDKDTTVES		KNDSTVD.TKEVAKDKLVAQAQTPDGTLAQMIVKSVT.KEQVN.A	NDKGQVD.NKEVAKDKLVAQAQTPDGTLAQMNVKSVI.KEQVN.A		90	/SA	:	
280	<i>I</i> DFVSTYDTVE	N	NN	N	N	H	R	AE	AD		AQTPDGTLAQ	AQTPDGTLAQ	*	330 340 350 360	SKLAKTKVKL\	е л	ב
270	TIGG-TVDIN	NDFVR.Y.T.	VDFVNAY.T.	VDFWNAY.T.		STT-GOSE	ATS	SANNOE.I	SANNOE.I		EVAKDKLVAQ	EVAKDIKLVAQ		35	DMDKKV-ENC	Ñ	
260	MIRGAK	Q.NGMIN	Q.NGAS	Q.NGAS	Q.NGAS	K.V.AG	K.V.TG	VV.PA	VV.PA		NDGTVD. TK	OKGQVD.NK		340	7/EAKQDGSA	.KD	
	:	:	:	:	:	:	:	:	:		2	N	:		VVKVGNEY		Z
						-								320	JEVQYVTEDSKTVVKVGNEY?EAKQDGSALMDKKV-ENGKLAKTKVKLVSA		<u>د</u>

 $--\dots$ TLSGDIQTAKGASQANNSAGYVDADGANKVIYDSTDNKYYQA.. ... TLSGDIQTAKGASQASSSASYVDADGNKVIYDSTDNKYYQV

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33 32 29 . . 722 M4071 11 11 K9 HSF API Rd 4223

ENGK. TE. KIGAKTS. IKEKDGKLFT. KANK. TNKVDG. NATEDA-DE GLV. AKDVID	. QGINEDNAFVKGLEKAASINKTKNAAVIVGDIANAVAQTPLTFAG-DT.TTKLGETLTI .QGINEDNAFIKGLENAAKDIKTKNAAVIVGDINAVAQTPLTFAG-DT.TTKLGETLTI ** *	390 390 400 STINPVKI SINVALIGIEDITJAVSFKQLKALQDKQVITSAS	S.QEENET	NNNENNNNNN	VNKAGMR.KTTGANNQAGQFETVTSGTNVTFDVNKAGMRVKTTGANGQNDFATVASGTNVTFDVNKAGMRVKTTGANGQNDFATVASGTNVTFD	KGGQTDINKLIDANIGVVAGTDGFTV. LAK. LININ. VN KGGQTDINKLIDANIGVVAGTDGFTV. LAK. LININ. VN
--	--	---	----------	------------	--	--

5,282

...NGDGKK----F.D..G.A.A....S.TATA..E...--EV

...AINGKK----..N..G.A.A....S.TAK-AEADTANGGEL

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33 32 29 K22 M4071 12 11 K9 HSF

NAYANGSSDADGGKATQTLGNDLNFKFKSTDSELLNIKAAGDTVTFTPKKGSVQVGDDGKAT. T.N. S.G. S.G. K.S.T. S.G. K.S.T. S.G. K.S.T. S.G. K.S.T. S.G. K.S.T. S.G. K.S.T. S.G. K.S.T. S.G. K.S.T. S.G. K.S.T. S.G. G. VEN. E. E. S.G. G. VEN. E. E. S.G. G. EN. I	470 480 490 500IQDGAKTTTGLVEASELVDSIANKLGANKVGVGKDGTGATSKNEEE.V.SELN.TDEEDSEN.TDEEDSE.
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	TVNNLLNIVQSNSGASLPFVVIDANGKPIN.TDGKPQKAIKGA	530 540 550 560 KVKQESTNETYVI.RDELIGVKSVEFKDTENGANGASTK	D. A.K. D. A.S.	A. S.Q.A. LT. ITLGTCNKE. A. S.Q.ALT. ITLGTCNKE. I. S.KDS.KKKDLTANG.TGSE I. S.KDS.KKKDLTANG.TGSE	ANGVP	570 580 590 600 ITKDGLTITPAND-ANGAAATDADKIKVASDGISAGNKAV
	NINNI	530 KVKQEGINFTY	D	A	\$	THADGI

FIG.28U

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...ADE-KE...A.....F...K.

. PANSAGOE..A....F....

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GGA.G.NT.NT.STK. N. GG.NN.NT.STK. DQS. N. GG.NN.NT.STK. DQS. GGA.G.NT.NT,STK. GGA.G.NT.NT,STK. YD. KP. D.DKL. L. HGKPLDAGHQV. LGNSDI

660	. D		TLINIKSTLP, I, TPNF, NA, AGQAQSLPSLSAAQQSN, S, K, V,
650 SKGKQTPTVADI	GAD. L.	GTDV GADL GADNN	OSLPSLSAAQQ
640 YKGLTINLDEK			NT.NA.AGQA
630 LONLTKQYDNA		D. D. CHTLANGTV. FEH. D. CHTLANGTV. FEH. XD.	KSTLP.I.TE
620 VANFINPLI'SSA	D.	1 • • (7) (7) 1	TT.T.
610 620 630 640 650 660 KNVVSGLKKFGDANFNPLTSSADNLTKQYDNAYKGLTNLDEKSKGKQTPTVADNTAATVGDL		T. GHILAN	

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VSGKTIDNGTREITFELAKDENAIAFGSGSKALRDNIVAIGTGNVANAEKSGAFGDPNYIED..

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FIG.28W

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G.28X	. VR	DGIMSNITVNITALAATDDDCAVVL.KAKD.KFYKA.DLMFN.SLKAGKSASDAKTPTGLSLVN **	SRDN.E.EE	FNA.KGST.DAVALNNLSKA.FKSKOGTTTTTTVSSDGISLQGK
FIG.28X	V	DGTMSNITVA ** *		



... GNOVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDT ... GNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDT ---TLSKDGLANGGKVISNNGKGTKDTDAANVQQLNEVRNLLGLGAAGANAAD... VDSSGQAKANTPVLSANGLDLOGKVISNVGKGTKDTDAANVQQINEVRNLLGLGVBGUNAD.. VVKSNEFTVRNADGSEINLVKVGDLYYSKEDIDPATSKPMICKTE----KYKVENGKVVSAN. VVKSNEFTVRNADGSETNLVKVGDLYYSKEDIDPATSKPMIGKTE-----KYKVENGKVVSAN VVKSNEFTVKETNÆKETSLVKVGDLYYSKEDIDLITIGQPKLKOGNIVAAKYQDKGGKVVS-V. VVKSNEFTVKETNGKETSLVKVGDLYYSKEDIDPATGKPKVINGNAVAAKYQDKDGKVVSAD. ...GSK-TEVILIMKGSGYVICAN ...GSSNTAVTL/INKGYGYVTGNQ .. TIDNIEATITNIKGSGYVICAQ-...GSK-TEVILIMKGSGYVTGNÇ

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FIG.28Z

VADALAKSGFEKGKADEADAKRAFDDKTKALSAGTTE-TVNAHDKVRFANGINIKVSAAT VADALAKSGFEKGKADAEKARARFGDETKALSSDKLE-TVNANDKVRFANGINIKVSAAT VADALAKSGFEKGKADAAEAEKAFAESAKDKQLSKOKAE-TVNAHDKVRFANGINIKVSAAT VADALAKSGFEKGKADAAEAEKAFAESAKOKQLSKOKAE-TVNAHDKVRFANGINIKVSAAT
EKLATGGIQVGVDKDGNANGDLSNVMVKTQKDGSKKALLATYNNAAGQTNVLINNPAEAIDRI EKLATGGVQVGVDDKDGNANGDLSNVMVKTQKDGSKKALLATYNNAAGQTNVLINNPAEAIDRI *
VESTDANGDKVITTFVKTDVELPLTQIYNIDANGKKITKVVVESTDANGDKVITTFVKTDVELPLTQIYNIDANGKKITKVVVESTDANGDKVITTFVKTDVELPLTQIYNIDANGKIV

API Rd 4223 LES-1 33 32 29 ...VESTDANGDKVITITFVKIDVELPLIQIYNIDANGAKI---V ...NEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQ-...NEQGIRFFHVNDGAQEPVVQGRNGIDSSASGKHSVAIGFQ AKADGEAAVAJGRQTQAGVQSIAJGDVAQATGDQSIAJGTGNVVAGKUSGAJGDPSTVKADN... KKADGKWYEI NADGIASN-KEVILCANDANGKKVVKVITENGADKWYYINADGAADKIKGEVS.. AKADGEAAVAIGRQTQAGAQSIAIGDNAQATGDQSIAIGTGAVVTGKHSGAIGDPSTVKADN.. KNGD-KWYYIKDDGSTIDMIKEVILCANDSDGAKNVKEDN----KWYGVKSDGSTDKTQVVEE. KKADGKWYEI NADGTASN-KEVILGNVDANGKKVVKVITENGADKWYYINADGAADKTKGEVS. $\mathsf{KDCQIIKWYELAMDGIADMIKEVIICANDSDCFGNVICINDG----KWYHAKADGIADKIIKGEND.$

FIG.28A



12 11 K9 HSF API API Rd 4223 LES-1

33 33 33 33 33

VTESNSVAL, SNSALSAGTHA, TQAK VTESNSVAL, SNSALSAGTHA, TQAK VTESNSVAL, SNSALSAGTHA, TQAK * * * * * * * * * * * * * * * * * * *		810 820 830 840 850 860 ETVIVKDKDKÆTTIVIVPKALGATVENSVYLGNKSTATIÓKGKNILKSDGTAGNTITAGTIGT	SYSVANINGSTDATQIDVFGVANNIT SYSVANINGSTDATQIDVFGVANNIT * * * * * * * * * * * * * * * * * * *	NDKVSTDEKHVVSLDPNDQSKGKGVV A-KVSTDEKHVVSLDPNDQSKGKGVV NDKVSTDEKHVVSLDPNDQSKGKGVV NDKVSTDEKHVVSLDPNDQSKGKGVV	
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	K Q V A X X X X X X X X X X X X X X X X X X	930 940 950 KVN T.P. P.
Ų	K. Q. K. Q. V. ***	0 920 930 940 950 VAKGVINLAGOVNKVEKRADAGIRSALAASQLPQASMSEKSM T. P. P. P. P. P. P. P. P. P. P. P. P. P. P

IG.28C'

990

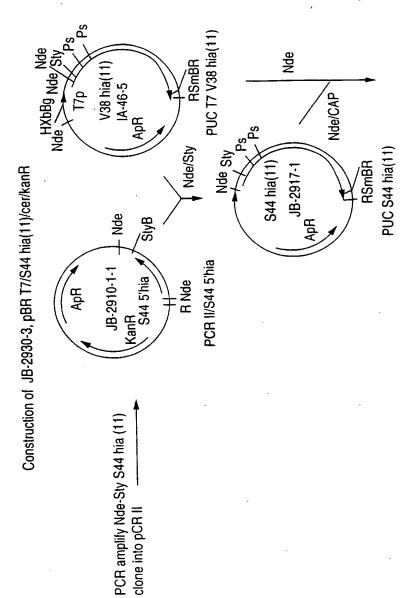
980

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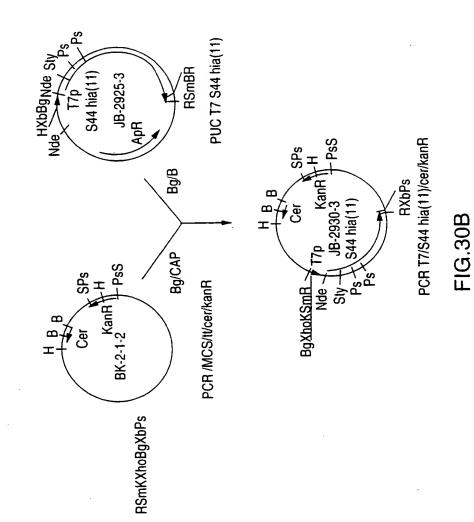
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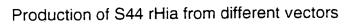
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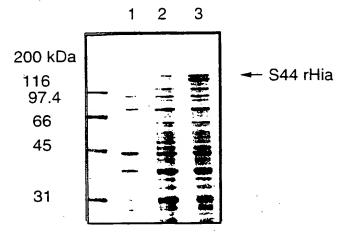


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 t_0

2. pET S44 hia

 t_4

3. pBR T7 S44 hia/cer/kanR t

FIG.31

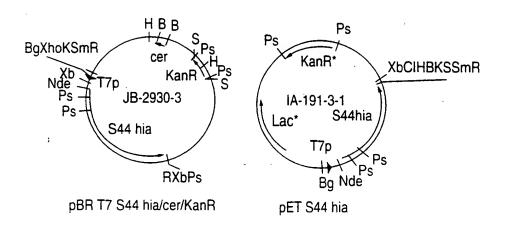


FIG.32